



Sequence Listing

<10> Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan l.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.

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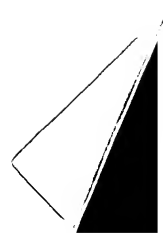
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tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200  
agggagtccc accatcgctg gtggtatccc agggtccttg ctcaagtttt 1250  
ctttgaaaag gagggctgga atggtacatc acataggcaa gtcttgccct 1300  
gtatttaggc tttgcctgct tgggtgatg taagggaat tgaaagactt 1350  
gcccattcaa aatgatcttt accgtggcct gcccattgct tatggtcccc 1400  
agcatttaca gtaacttgtg aatgttaagt atcatctctt atctaaatat 1450  
taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaa 1508

<210> 10  
<211> 319  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-17  
<223> Signal Peptide

<220>  
<221> misc\_feature  
<222> 36-47, 108-113, 166-171,198-203, 207-212  
<223> N-myristoylation Sites.

<220>  
<221> misc\_feature  
<222> 39-42  
<223> Glycosaminoglycan Attachment Site.

<220>  
<221> TRANSMEM  
<222> 136-152  
<223> Transmembrane Domain

<220>  
<221> misc\_feature  
<222> 161-163, 187-190 and 253-256  
<223> N-glycosylation Sites.

<400> 10  
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu  
1 5 10 15  
  
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys  
20 25 30  
  
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
35 40 45  
  
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
50 55 60  
  
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
65 70 75  
  
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
80 85 90  
  
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
95 100 105  
  
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
110 115 120



Pro Thr Asp Trp	Leu Thr Leu Glu Asp	Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe	Gly Leu Ile Ser Val	Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys	Ala Gln Gly Arg Val	Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu	Ala Ile Val Gly Gly	Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu	Gly Phe Asn Asp Ser	Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn	305	310	315
Pro Lys Ala Val					

<210> 11

<211> 2720

<212> DNA

<213> Homo sapiens

<400> 11

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gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150

gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300  
gctttttctgt ggactcctct tctacatcaa cttggctgac cattggaaaag 350  
ctctggccttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
gggttaaaac cagcaaattcc acccgtctta ccagctcctc agaaggcgga 450  
caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
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catggaaaag ataccgcaag tttgcatggg gccatgacga gctgaagcct 850  
gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900  
cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950  
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ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100  
atcggctaata gcctgccttc agaacaccat ccaagattcc ttactcggat 1150  
gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200  
cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300  
cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350  
caatacccac agtggcctct tcacccacct gggcgtattc acgctgggcg 1400  
ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450  
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tgcttcctgc cagggacgct ggctctgggc gtctaccacg gcctgccccg 1650

cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
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 tacccccagc cgggccgtcg ggacgtggag gtcaagccag cagacaggca 1800  
 caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850  
 tcacagggga cgcgaaatac caggactggg gctgggagat tctgcagagc 1900  
 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950  
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
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 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250  
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 cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350  
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 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450  
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctgaagc 2500  
 ctcagatgtc cccaatcaa gggctctggag gggctgccgt gactccagag 2550  
 gcctgaggct ccagggctgg ctctggtgtt tacaagctgg actcagggat 2600  
 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser

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Gln Ser Asp Phe	Leu Thr Pro Pro Val	Gly Gly Ala Pro Trp	Ala
	20	25	30
Val Ala Thr Thr	Val Val Met Tyr Pro	Pro Pro Pro Pro Pro	Pro
	35	40	45
His Arg Asp Phe	Ile Ser Val Thr Leu	Ser Phe Gly Glu Ser	Tyr
	50	55	60
Asp Asn Ser Lys	Ser Trp Arg Arg Arg	Ser Cys Trp Arg Lys	Trp
	65	70	75
Lys Gln Leu Ser	Arg Leu Gln Arg Asn	Met Ile Leu Phe Leu	Leu
	80	85	90
Ala Phe Leu Leu	Phe Cys Gly Leu Leu	Phe Tyr Ile Asn Leu	Ala
	95	100	105
Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln	Lys
	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro	Val
	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu	Pro
	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly	Pro
	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp	Gly
	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp	Pro
	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg	Gly
	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg	Arg
	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr	Gln
	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile	Asp
	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp	Gly
	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp	Phe
	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp	Ile

290					295					300				
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser
				305					310					315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu
				320					325					330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu
				335					340					345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn
				350					355					360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser
				365					370					375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr
				380					385					390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe
				395					400					405
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
				500					505					510
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val

	575		580		585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro Glu	Thr		
	590	595	600		
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys		
	605	610	615		
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe		
	620	625	630		
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln		
	635	640	645		
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe		
	650	655	660		
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp		
	665	670	675		
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu	Ala		
	680	685	690		
His Pro Leu Pro	Ile Trp Thr Pro Ala				
	695				

<210> 13  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 13  
 cgccagaagg gcgtgattga cgtc 24

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 14  
 ccataccttct tcccagacag gccg 24

<210> 15  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tocaggtoct tcagtgagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100  
gcgcagctgc cctgggagga cggcaggctc gggttgctct ccggcggcct 150  
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200  
gtttctttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250  
cgggcagtca ggggacaagg gcaggagacc tcgggcccctc ccgctgcctg 300  
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
cccaccgcct ggcagtgtct gtgcccttcc gcgaacgctt cgaggagctc 400  
ctggctcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450  
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500  
cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550  
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
tggttttctt gaggtgggc ccttccacgt ggctccccg gagctccacc 650  
ctctctacca ctacaagacc tatgtggcg gcactctgct gctctccaag 700  
cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750  
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800  
ttttccgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850  
catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900  
acaggagcag ttcaagggtg acagggaggg aggcctgaac actgtgaagt 950  
accatgtggc ttcccgact gccctgtctg tgggcggggc ccctgcact 1000  
gtcctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050  
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ggccgccaag gcaggcttgg gctgggccag gacacgtggg gtgcctggga 1250

cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300  
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 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400  
 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450  
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 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17  
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp  
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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
                   20                  25                  30  
  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
                   35                  40                  45



Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala	
				50					55					60	
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys	
				65					70					75	
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	
				80					85					90	
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	
				95					100					105	
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser	
				110					115					120	
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp	
				125					130					135	
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu	
				140					145					150	
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp	
				155					160					165	
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala	
				170					175					180	
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His	
				185					190					195	
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His	
				200					205					210	
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly	
				215					220					225	
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu	
				230					235					240	
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe	
				245					250					255	
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg	
				260					265					270	
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly	
				275					280					285	
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu	
				290					295					300	
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp	
				305					310					315	
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser				
				320					325						

<210> 18  
<211> 23  
<212> DNA  
<<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 18  
gcgaacgctt cgaggagtcc tgg 23

<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50  
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150  
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagatagga acagaagagg gtagtggggtg 300  
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc\_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly  
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24

<211> 616

<212> PRT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-33

<223> Signal peptide.

<220>

<221> TRANSMEM

<222> 13-40

<223> Transmembrane domain (type II).

<400> 24

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				20					25					30	
Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Leu	Pro	Ala	Gly	Cys	Lys	His	
				35					40					45	
Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	
				50					55					60	
Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro	
				65					70					75	
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn	
				80					85					90	
Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
				95					100					105	
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	
				110					115					120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
				125					130					135	
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	
				140					145					150	
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
				155					160					165	
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	
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Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	
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Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	
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Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	
				215					220					225	
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	
				230					235					240	
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	
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Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
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Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	
				275					280					285	

Thr Asp Glu Ser	Gln Gly Ile Phe Val	Glu Lys Asn Met Ile His
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Asn Cys Ser Leu	Ile Ala Ser Ala Leu	Thr Ile Ser Asn Ile Gln
	305	310 315
Ala Gly Ser Thr	Gly Asn Trp Gly Cys	His Val Gln Thr Lys Arg
	320	325 330
Gly Asn Asn Thr	Arg Thr Val Asp Ile	Val Val Leu Glu Ser Ser
	335	340 345
Ala Gln Tyr Cys	Pro Pro Glu Arg Val	Val Asn Asn Lys Gly Asp
	350	355 360
Phe Arg Trp Pro	Arg Thr Leu Ala Gly	Ile Thr Ala Tyr Leu Gln
	365	370 375
Cys Thr Arg Asn	Thr His Gly Ser Gly	Ile Tyr Pro Gly Asn Pro
	380	385 390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly Phe
	395	400 405
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp Val
	410	415 420
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu Thr
	425	430 435
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val Glu
	440	445 450
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala Glu
	455	460 465
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser Lys
	470	475 480
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met Leu
	485	490 495
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys Ala
	500	505 510
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr Arg
	515	520 525
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn Ile
	530	535 540
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly Met
	545	550 555
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr Gly
	560	565 570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys  
575 580 585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu  
590 595 600

Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr  
605 610 615

Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

gaggactcac caatctggtt cggc 24

<210> 26

<211> 24

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 26

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<210> 27

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 27

gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgaaggag ttatcagaga cattgagagg caaattcgga 150



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<210> 29

<211> 81

<212> PRT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-21

<223> Signal peptide.

<400> 29

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Thr	Ala	Ala	Thr	Val	Ala	Gly	Val	His	Val	Lys	Gln	Gln	Trp	Asp
			20						25				30	

Gln	Gln	Arg	Leu	Arg	Asp	Gly	Val	Ile	Arg	Asp	Ile	Glu	Arg	Gln
			35						40				45	

Ile	Arg	Lys	Lys	Glu	Asn	Ile	Arg	Leu	Leu	Gly	Glu	Gln	Ile	Ile
			50						55				60	

Leu	Thr	Glu	Gln	Leu	Glu	Ala	Glu	Arg	Glu	Lys	Met	Leu	Leu	Ala
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Lys	Gly	Ser	Gln	Lys	Ser
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<210> 30

<211> 2128

<212> DNA

<213> Homo sapiens

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<210> 31

<211> 322

<212> PRT

<213> Homo sapiens

<400> 31

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Ser	Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg	20	25	30	
Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	35	40	45	
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	50	55	60	
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	65	70	75	
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	80	85	90	
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	95	100	105	

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu	Ser Ala Ser Ile Ile Tyr	110	115	120
Pro Thr Thr Tyr	Val Gln Phe Leu Ser	His Gly Arg Ser Arg Asp	125	130	135
His Ala Ile Ala	Ala Thr Phe Phe Ser	Cys Ile Ala Cys Val Ala	140	145	150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg	Ala Arg Pro Gly Glu Ile	155	160	165
Thr Gly Tyr Met	Ala Thr Val Pro Gly	Leu Leu Lys Val Leu Glu	170	175	180
Thr Phe Val Ala	Cys Ile Ile Phe Ala	Phe Ile Ser Asp Pro Asn	185	190	195
Leu Tyr Gln His	Gln Pro Ala Leu Glu	Trp Cys Val Ala Val Tyr	200	205	210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile	Ala Ile Leu Leu Asn Leu	215	220	225
Gly Glu Cys Thr	Asn Val Leu Pro Ile	Pro Phe Pro Ser Phe Leu	230	235	240
Ser Gly Leu Ala	Leu Leu Ser Val Leu	Leu Tyr Ala Thr Ala Leu	245	250	255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp	Glu Lys Tyr Gly Gly Gln	260	265	270
Pro Arg Arg Ser	Arg Asp Val Ser Cys	Ser Arg Ser His Ala Tyr	275	280	285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu	Ala Val Ala Ile Leu Thr	290	295	300
Ala Ile Asn Leu	Leu Ala Tyr Val Ala	Asp Leu Val His Ser Ala	305	310	315
His Leu Val Phe	Val Lys Val		320		

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
			35						40				45	
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
			50						55				60	
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
			65						70				75	
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
			80						85				90	
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
			95						100				105	
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
			110						115				120	

Phe Ser Ser Tyr	Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg	125	130	135
Phe Ala Ala Gly	Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	140	145	150
Leu Arg Ala Trp	Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp	155	160	165
Ser Tyr Asp Glu	Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala	170	175	180
Gly Gln Leu Pro	Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	185	190	195
His Arg Phe Ser	Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu	200	205	210
Ser Asp Cys Ser	Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser	215	220	225
Leu Cys Ser Leu	Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu	230	235	240
Ala Ser Gln Leu	Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro	245	250	255
Pro Ser Arg Glu	Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu	Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu	Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu	Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser	Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
Glu Pro Glu Glu	Gln	335		

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

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<210> 36  
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<400> 36  
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<210> 37  
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<400> 37  
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<210> 38  
<211> 39  
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<400> 38  
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<210> 40  
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<212> DNA

<213> Homo sapiens

<400> 40

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<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

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Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn
				20					25					30
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
				35					40					45
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
				50					55					60
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
				65					70					75
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
				80					85					90
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
				95					100					105

Ile Ser Thr Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val
	110					115					120
Pro Trp Asn Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser
	125					130					135
Ala His Pro Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr
	140					145					150
Trp Ser Leu Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser
	155					160					165
Ile Thr Val Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val
	170					175					180
Thr Pro Leu Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser
	185					190					195
Asp Ser Phe Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
	200					205					210
Gln Pro Thr Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
	215					220					225
Thr Ser Asp Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
	230					235					240
Gly Ala Ile Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
	245					250					255
Val Gly Tyr Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
	260					265					270
His Arg Arg Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
	275					280					285
Asp Asn Ala Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
	290					295					300
Tyr Tyr Asn Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
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Glu Asn Ala Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
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<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

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ccctataata aattttactc tatacaaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20						25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35						40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
			50						55					60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65						70					75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80						85					90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95						100					105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110						115					120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125						130					135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140						145					150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155						160					165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170						175					180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185						190					195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200						205					210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215						220					225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

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Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile					
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<210> 45  
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<400> 48

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<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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<210> 50  
<211> 283  
<212> PRT  
<213> Homo sapiens

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Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
35 40 45  
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
50 55 60  
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
65 70 75  
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

	80	85	90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala	95	100	105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln	110	115	120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys	125	130	135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe	140	145	150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala	155	160	165
Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr	170	175	180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp	185	190	195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys	200	205	210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro	215	220	225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu	230	235	240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly	245	250	255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro	260	265	270
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Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
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Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
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Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
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Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
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Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
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				230					235					240

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Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His	320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly	335	340	345
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Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser	365	370	375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser	410	415	420
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<212> DNA

<213> Homo sapiens

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<211> 280

<212> PRT

<213> Homo sapiens

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Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150



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Val Thr Gln Gly	Glu Glu Gly Gly Asp	Pro Ala Gln Leu Leu Glu
	170	175 180
Ile Leu Cys Ser	Gln Leu Cys Pro His	Gly Ala Gln Ala Leu Ala
	185	190 195
Leu Gly Arg Glu	Phe Cys Gln Arg Lys	Ser Pro Gly Ala Val Arg
	200	205 210
Ala Leu Leu Pro	Glu Glu Thr Pro Ala	Ala Val Leu Ser Ser Ala
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Glu Asn Ile Ala	Val Gly Leu Ala Thr	Glu Lys Ala Cys Ala Trp
	230	235 240
Leu Ser Ala Asn	Ile Thr Ala Leu Ile	Arg Arg Glu Val Lys Ala
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His Val Tyr Gly	Met Val Pro Pro Asn	Tyr Cys Ser Gln Arg Pro			
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Arg Leu Gln Arg	Met Pro Tyr His Tyr	Tyr Glu Pro Lys Gly Pro			
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Asp Glu Cys Val	Thr Tyr Ile Gln Asn	Glu His Ser Arg Lys Gly			
	260		265		270
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<210> 58

<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala
				20					25					30
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
				35					40					45
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
				50					55					60
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
				65					70					75
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
				80					85					90

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln	95	100	105
Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala	110	115	120
Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln	125	130	135
His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys	140	145	150
His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val	155	160	165
Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met	170	175	180
Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu	185	190	195
Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val	200	205	210
Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr	215	220	225
Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile	230	235	240
Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser	245	250	255
Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser	260	265	270
Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala	365	370	375



Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln	575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp	590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile	605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg	620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys	635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly	
				665						670				675	
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu	
				680						685				690	
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr	
				695						700				705	
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr	
				710						715				720	
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met	
				725						730				735	
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr	
				740						745				750	
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys	
				755						760				765	
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His	
				770						775				780	
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn	
				785						790				795	
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr	
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Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro	
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Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	
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Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	
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Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860						865				870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875						880				885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
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Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905						910				915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920						925				930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935						940				945	

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu		
	950	960
Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His		
	965	975
Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly		
	980	990
Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro		
	995	1005
Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys		
	1010	1020
Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg		
	1025	1035
Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro		
	1040	1050
Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu		
	1055	1065
Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp		
	1070	1080
Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly		
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Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr		
	1100	1110
Pro Pro Leu Thr Ile		
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<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

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<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgctg gagc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe.

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<210> 62  
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<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
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<210> 63  
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 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

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 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg  
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 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala  
 35 40 45  
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val  
 50 55 60

Pro	Ser	Ala	Leu	Thr 65	Thr	Pro	Gly	Leu	Thr 70	Thr	Pro	Gly	Thr	Pro 75
Lys	Thr	Leu	Asp	Leu 80	Arg	Gly	Arg	Ala	Gln 85	Ala	Leu	Met	Arg	Ser 90
Phe	Pro	Leu	Val	Asp 95	Gly	His	Asn	Asp	Leu 100	Pro	Gln	Val	Leu	Arg 105
Gln	Arg	Tyr	Lys	Asn 110	Val	Leu	Gln	Asp	Val 115	Asn	Leu	Arg	Asn	Phe 120
Ser	His	Gly	Gln	Thr 125	Ser	Leu	Asp	Arg	Leu 130	Arg	Asp	Gly	Leu	Val 135
Gly	Ala	Gln	Phe	Trp 140	Ser	Ala	Ser	Val	Ser 145	Cys	Gln	Ser	Gln	Asp 150
Gln	Thr	Ala	Val	Arg 155	Leu	Ala	Leu	Glu	Gln 160	Ile	Asp	Leu	Ile	His 165
Arg	Met	Cys	Ala	Ser 170	Tyr	Ser	Glu	Leu	Glu 175	Leu	Val	Thr	Ser	Ala 180
Glu	Gly	Leu	Asn	Ser 185	Ser	Gln	Lys	Leu	Ala 190	Cys	Leu	Ile	Gly	Val 195
Xaa	Gly	Gly	His	Ser 200	Leu	Asp	Ser	Ser	Leu 205	Ser	Val	Leu	Arg	Ser 210
Phe	Tyr	Val	Leu	Gly 215	Val	Arg	Tyr	Leu	Thr 220	Leu	Thr	Phe	Thr	Cys 225
Ser	Thr	Pro	Trp	Ala 230	Glu	Ser	Ser	Thr	Lys 235	Phe	Arg	His	His	Met 240
Tyr	Thr	Asn	Val	Ser 245	Gly	Leu	Thr	Ser	Phe 250	Gly	Glu	Lys	Val	Val 255
Glu	Glu	Leu	Asn	Arg 260	Leu	Gly	Met	Met	Ile 265	Asp	Leu	Ser	Tyr	Ala 270
Ser	Asp	Thr	Leu	Ile 275	Arg	Arg	Val	Leu	Glu 280	Val	Ser	Gln	Ala	Pro 285
Val	Ile	Phe	Ser	His 290	Ser	Ala	Ala	Arg	Ala 295	Val	Cys	Asp	Asn	Leu 300
Leu	Asn	Val	Pro	Asp 305	Asp	Ile	Leu	Gln	Leu 310	Leu	Lys	Asn	Gly	Gly 315
Ile	Val	Met	Val	Thr 320	Leu	Ser	Met	Gly	Val 325	Leu	Gln	Cys	Asn	Leu 330
Leu	Ala	Asn	Val	Ser 335	Thr	Val	Ala	Asp	His 340	Phe	Asp	His	Ile	Arg 345

Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp
350	355	360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr
365	370	375
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu
380	385	390
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg
395	400	405
Gln Val Glu Lys	Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val
410	415	420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser
425	430	435
His Leu Val Pro	Gln Asn Gly His Gln	Ala Thr His Leu Glu Val
440	445	450
Thr Lys Gln Pro	Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala
455	460	465
Ser Pro Tyr Leu	Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro
470	475	480
Thr Phe Thr Gln	Trp Leu Cys	
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<210> 64

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 66

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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<210> 68  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
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 35 40 45  
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
 50 55 60  
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
 65 70 75  
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
 80 85 90  
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
 95 100 105  
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
 110 115 120  
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
 125 130 135  
 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
 140 145 150  
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
 155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
170 175 180

Met Leu Ser

<210> 69

<211> 3170

<212> DNA

<213> Homo sapiens

<400> 69

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tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150  
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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met	Ala	Ala	Leu	Met	Arg	Ser	Lys	Asp	Ser	Ser	Cys	Cys	Leu	Leu
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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45
Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly
				50					55					60
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala
				65					70					75
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys
				80					85					90
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg
				95					100					105
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr
				110					115					120

Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
				125					130					135
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140					145					150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155					160					165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170					175					180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185					190					195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200					205					210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215					220					225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230					235					240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
				245					250					255

Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200  
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 ctgaaaaga 1809

<210> 72  
 <211> 363  
 <212> PRT  
 <213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

275										280					285				
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln					
				290					295					300					
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn					
				305					310					315					
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr					
				320					325					330					
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg					
				335					340					345					
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp					
				350					355					360					

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 73  
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<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 74  
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<210> 75  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 75  
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<210> 76  
 <211> 1989  
 <212> DNA  
 <213> Homo sapiens



<400> 76

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ccactctcag cccccacat ttgcatctgc tgggtggacct gccaccatca 1950  
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu	35	40	45	
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro	50	55	60	
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val	65	70	75	
Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His	80	85	90	
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His	95	100	105	
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg	110	115	120	
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro	125	130	135	

Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu	140	145	150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp	155	160	165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu	170	175	180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala	185	190	195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser	200	205	210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val	215	220	225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln	230	235	240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu	245	250	255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu	260	265	270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn	275	280	285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg	290	295	300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu	305	310	315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp	320	325	330
Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys					335	340	

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

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Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	
Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120	
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135	

Leu Ala Ser Leu	Thr Val Ile Leu Ala	Ile Phe Met Val Ile Thr
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Ala Leu Val Lys	Val Asp Thr Ser Ser	Trp Thr Arg Gly Phe Phe
	155	160 165
Ala Val Thr Ile	Val Cys Met Val Ile	Leu Ser Gly Ala Ser Thr
	170	175 180
Val Phe Ser Ser	Ser Ile Tyr Gly Met	Thr Gly Ser Phe Pro Met
	185	190 195
Arg Asn Ser Gln	Ala Leu Ile Ser Gly	Gly Ala Met Gly Gly Thr
	200	205 210
Val Ser Ala Val	Ala Ser Leu Val Asp	Leu Ala Ala Ser Ser Asp
	215	220 225
Val Arg Asn Ser	Ala Leu Ala Phe Phe	Leu Thr Ala Thr Ile Phe
	230	235 240
Leu Val Leu Cys	Met Gly Leu Tyr Leu	Leu Leu Ser Arg Leu Glu
	245	250 255
Tyr Ala Arg Tyr	Tyr Met Arg Pro Val	Leu Ala Ala His Val Phe
	260	265 270
Ser Gly Glu Glu	Glu Leu Pro Gln Asp	Ser Leu Ser Ala Pro Ser
	275	280 285
Val Ala Ser Arg	Phe Ile Asp Ser His	Thr Pro Pro Leu Arg Pro
	290	295 300
Ile Leu Lys Lys	Thr Ala Ser Leu Gly	Phe Cys Val Thr Tyr Val
	305	310 315
Phe Phe Ile Thr	Ser Leu Ile Tyr Pro	Ala Val Cys Thr Asn Ile
	320	325 330
Glu Ser Leu Asn	Lys Gly Ser Gly Ser	Leu Trp Thr Thr Lys Phe
	335	340 345
Phe Ile Pro Leu	Thr Thr Phe Leu Leu	Tyr Asn Phe Ala Asp Leu
	350	355 360
Cys Gly Arg Gln	Leu Thr Ala Trp Ile	Gln Val Pro Gly Pro Asn
	365	370 375
Ser Lys Ala Leu	Pro Gly Phe Val Leu	Leu Arg Thr Cys Leu Ile
	380	385 390
Pro Leu Phe Val	Leu Cys Asn Tyr Gln	Pro Arg Val His Leu Lys
	395	400 405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser
	410	415 420

Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu  
425 430 435

Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly  
440 445 450

Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser  
455 460 465

Ala Cys Ser Thr Leu Leu Val His Leu Ile  
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<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 80

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<210> 81

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 81

cgtaggtgac acagaagccc agg 23

<210> 82

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 82

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<210> 83

<211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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<210> 84  
<211> 567  
<212> PRT  
<213> Homo sapiens

<400> 84  
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Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
35 40 45  
Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
50 55 60  
Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
65 70 75  
Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
80 85 90  
Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
95 100 105  
Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
110 115 120  
His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
125 130 135  
Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
140 145 150  
Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
155 160 165  
Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
170 175 180  
Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
185 190 195

Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His	Thr
200		205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro	Ala
215		220	225
Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe	Tyr
230		235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala	His Ser Cys Leu Ser	Asp
245		250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu	Pro
260		265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn	Ala
275		280	285
Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val	Gln
290		295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys	Ala
305		310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg	Ile
320		325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu	Arg
335		340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe	Arg
350		355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser	Asn
365		370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg	Glu
380		385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala	Ala
395		400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala	Leu
410		415	420
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu	Trp
425		430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His	Ser
440		445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr	Glu
455		460	465
Lys Asp Asp Trp	Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala	Gly
470		475	480

Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
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Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
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<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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			20						25				30	

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	35	40	45
Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile	50	55	60
Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys	65	70	75
Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg	80	85	90
Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val	95	100	105
Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn	110	115	120
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu	125	130	135
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu	140	145	150
Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys	155	160	165
Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His	170	175	180
Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala	185	190	195
Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr	200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu	215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile	230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu	245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro	260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu	275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe	290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys	305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr			

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His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
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Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
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Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
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Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
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Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
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Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
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Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
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Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
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Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
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Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
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Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
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Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
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Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
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Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
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Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
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Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	

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Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly					
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Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile					
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Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser					
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Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly					
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Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu					
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His Ile Gln Asp

<210> 87

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 87

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<210> 88
<211> 660
<212> PRT
<213> Homo sapiens

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                      20                      25                      30

Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
                      35                      40                      45

Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
                      50                      55                      60

Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
                      65                      70                      75

Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
                      80                      85                      90

Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
                      95                      100                      105

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Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu	110	115	120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val	125	130	135
Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390

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Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu	
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Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly	
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Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys	
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Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg	
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Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val	
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Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val	
				515					520					525	
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala	
				530					535					540	
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu	
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Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr	
				560					565					570	
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp	
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Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp	
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Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe	
				605					610					615	
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro	
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Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu	
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<212> DNA  
<213> Artificial Sequence

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<400> 94

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<211> 307

<212> PRT

<213> Homo sapiens

<400> 95

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Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His
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Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser
				65					70					75
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser
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Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His
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Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu
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Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp
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Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu
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Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala
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				170					175					180
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser
				185					190					195
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His
				200					205					210



Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr
				215					220					225
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Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
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Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
				260					265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
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Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
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<210> 97  
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 <213> Artificial Sequence

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<400> 97  
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<210> 98  
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 <212> DNA  
 <213> Artificial Sequence

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<210> 99  
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<212> DNA

<213> Homo sapiens

<400> 99

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gaaatgtact aaataaaatg tacatctga 1429

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<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
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Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
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Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
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Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
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Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
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Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
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Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
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Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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				215					220					225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser

230	235	240
Glu Val Val Leu Asp Ser Lys Arg Gln	Val Glu Lys Glu Glu Thr	
245	250	255
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260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val	Val Glu Asp Arg Pro Val	
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly	Glu Leu Gly Gln Thr Pro	
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Gln Val Gln Ala Ala Leu Ser Val Ser	Gln Glu Asn Pro Glu Met	
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Glu Gly Pro Glu Arg Asp Gln Leu Val	Ile Pro Asp Gly Gln Glu	
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly	Arg Asn Gln Gln Lys Leu	
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Arg Gly Glu Asp Asp Tyr Asn Met Asp	Glu Asn Glu Ala Glu Ser	
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala	Gly Asn Asp Arg Asn Ile	
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys	Arg Asp Thr Ile Asn Leu	
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Leu Asp Gln Arg Glu Lys Arg Asn His	Thr Leu	
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<210> 101  
 <211> 3671  
 <212> DNA  
 <213> Homo sapiens

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 <211> 1089  
 <212> PRT  
 <213> Homo sapiens

<400> 102  
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 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro  
 35 40 45  
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala  
 50 55 60  
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile  
 65 70 75  
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val  
 80 85 90  
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser  
 95 100 105  
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu  
 110 115 120  
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu  
 125 130 135  
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly  
 140 145 150  
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys  
 155 160 165

Gln Leu Thr Ser	Ala Gly Arg Arg Val	Val Phe Met Gly Asp Asp
	170	175 180
Thr Trp Lys Asp	Leu Phe Pro Gly Ala	Phe Ser Lys Ala Phe Phe
	185	190 195
Phe Pro Ser Phe	Asn Val Arg Asp Leu	Asp Thr Val Asp Asn Gly
	200	205 210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp Asp
	215	220 225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His Lys
	230	235 240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln Met
	245	250 255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp Thr
	260	265 270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly Asp
	275	280 285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe Leu
	290	295 300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu Pro
	305	310 315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu Leu
	320	325 330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met Ala
	335	340 345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser Ala
	350	355 360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val Ser
	365	370 375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln Ala
	380	385 390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser Ala
	395	400 405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala Thr
	410	415 420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly Ala
	425	430 435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val Arg
	440	445 450



Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys	455	460	465
Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys	470	475	480
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	485	490	495
Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	500	505	510
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	515	520	525
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	530	535	540
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	545	550	555
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	560	565	570
Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	575	580	585
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	590	595	600
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	605	610	615
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	620	625	630
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	635	640	645
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	650	655	660
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	665	670	675
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	680	685	690
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	695	700	705
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	710	715	720
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	725	730	735

Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp Tyr	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met	Gln Glu Glu Phe Arg Gly	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	1010	1015	1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg  
1025 1030 1035

Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe  
1040 1045 1050

Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly  
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Arg Gln Leu Phe Leu Ala Gln Gln Arg  
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<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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cttatccatc aacatgaaga atgtctaca atggactcca ccagagggtc 150

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<210> 104  
<211> 442  
<212> PRT  
<213> Homo sapiens

<400> 104  
Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys  
1 5 10 15  
Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu  
20 25 30  
Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr  
35 40 45  
Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser  
50 55 60  
Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu  
65 70 75  
Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His  
80 85 90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile
				170					175					180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys
				185					190					195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys
				200					205					210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val
				215					220					225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro
				230					235					240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu
				245					250					255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser
				260					265					270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys
				275					280					285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys
				290					295					300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser
				305					310					315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu
				320					325					330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp
				335					340					345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro
				350					355					360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr
				365					370					375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser  
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly  
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro  
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly  
425 430 435

Leu Tyr Val Gln Met Glu Asn  
440

<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

cgctgctgct gttgctcctg g 21

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

cagtgtgccca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtcgcaggc agcgttgg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108  
ctcctccgag tctgtgtgct cctgc 25

<210> 109

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

cggacgcgtg ggccggacgcg tgggcccgcg cgtgggtctc tgcggggaga 50

cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgtgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150

gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200

aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttcctgctg cgagcccgct ggggtgggtctc ggccgcccac tgcttcagcc 300

acagagacct ccgcactggc ctggtggtgc tgggcgcccac cgtcctgagt 350

actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400

ccccgactac caccatga cccacgcca cgacatctgc ctgctgcggc 450

tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500

gggagaaggg ccaggccccc cacagcgggg acacggtgcc ggggtggctgg 550

ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600

ccaaggctcg agtgtggac ccggacgtct gcaacagctc ctggaagggc 650

cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700

gggcttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750

ctcacggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800

ccgcagctgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850

ggttcggcgg agcagtcctc agcccggccc cctgcctggg accaccaggc 900

ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
 gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000  
 tggttcagggt tgggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
 tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100  
 aaaaaaaaaa gaaa 1114 '

<210> 111  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 111  
 Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
 1 5 10 15  
 Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
 20 25 30  
 Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
 35 40 45  
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
 50 55 60  
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
 65 70 75  
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
 80 85 90  
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
 95 100 105  
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
 110 115 120  
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
 125 130 135  
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
 140 145 150  
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
 155 160 165  
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
 170 175 180  
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
 185 190 195  
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg



	200	205	210
Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg	215	220	225
Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly	230	235	240
Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val	245	250	255
Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly	260	265	270
Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala	275	280	

<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 112  
 gacgtctgca acagctcctg gaag 24

<210> 113  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 113  
 cgagaaggaa acgaggccgt gag 23

<210> 114  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 114  
 tgacattac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115  
 <211> 1808  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
 gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50

cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100  
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
tatgtcaccc gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200  
ggtcacgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250  
aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
tgtcaacgcc cggcacctgg acttggttc cctcaagtct atccgagagt 400  
ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450  
aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500  
gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550  
tgctggacaa gctgaaagcc tcagcccctt cgcgatcat caacctctcg 600  
tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650  
gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700  
tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750  
actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800  
cacgggcac catggctcca ccttctccag caccacactc gggcccatct 850  
tctggctgct ggtcaagagc ccgagctgg ccgcccagcc cagcacatac 900  
ctggccgtgg cggaggaact ggcggatgtt tccggaagt acttcgatgg 950  
actcaaacag aaggccccgg cccccaggc tgaggatgag gaggtggccc 1000  
ggaggctttg ggctgaaagt gcccgcctgg tgggcttaga ggctccctct 1050  
gtgaggggagc agcccctccc cagataacct ctggagcaga tttgaaagcc 1100  
aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgcagcttc 1150  
ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200  
agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250  
gcactgcccc gggctctggc tggttccgtc tgctctgctg ccagcagggg 1300  
agagggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350  
ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcgg 1400  
gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450

tctgacactt ggtggattct tgggtccctg tgggaccttg tgcattgcatg 1500  
gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550  
ctgtctccca tgatggtgtg gtacagcgag ctgttgctctg gctatggcat 1600  
ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650  
gagagcaggt gcaggtgtca tcccaggttc aggctctgca cggcatggag 1700  
tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750  
caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800  
gctcattt 1808

<210> 116  
<211> 331  
<212> PRT  
<213> Homo sapiens

<400> 116  
Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala  
1 5 10 15  
Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
20 25 30  
Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
35 40 45  
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
50 55 60  
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
65 70 75  
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
80 85 90  
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
95 100 105  
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
110 115 120  
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
125 130 135  
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
140 145 150  
Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
155 160 165  
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
170 175 180

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn
				185					190					195
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe
				200					205					210
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val
				215					220					225
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttcgcg agcgctggca tgtggtcctg gggcgcggtt ggcggcgctg 50  
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100  
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150  
 agcgccggtt gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200  
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcatctt actctcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400  
 tccagccttt gaggacctt agggagcagc aagggccctg atgcggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccagg tgtctttcag 500  
 agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550  
 ttctctcaca ggggatgact gcttccaagt tggcaagggtg gcctatgaca 600  
 tgggggatta ttacatgcc attccatggc tggaggaggc tgtcagtctc 650  
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700  
 agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750  
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
 cccaaccac gtggtagctg aggtgtcat ccaggagccc aatatacccc 900  
 aactgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
 cagccactc tctaccagat ccttagcctc tactgttct atgagacca 1000  
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050  
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100  
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150  
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
 ggctgaagga cactgttgac ccaaaactgg tgaccctcaa ccaccgcatt 1250  
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450  
 cttcatctat gccaacctca gcgtgcctgt ggttaggaat gcagcactgt 1500  
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550  
 gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600  
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700  
 aagccaggag ccaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaa tcagaggcaa 1800  
 gggagaggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850

agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900  
ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950  
acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000  
cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100  
agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150  
tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200  
tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	1	5	10	15
Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	20	25	30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	

Gly Asp Asp Cys	Phe Gln Val Gly Lys	Val Ala Tyr Asp Met	Gly
185	190		195
Asp Tyr Tyr His	Ala Ile Pro Trp Leu	Glu Glu Ala Val Ser	Leu
200	205		210
Phe Arg Gly Ser	Tyr Gly Glu Trp Lys	Thr Glu Asp Glu Ala	Ser
215	220		225
Leu Glu Asp Ala	Leu Asp His Leu Ala	Phe Ala Tyr Phe Arg	Ala
230	235		240
Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu	Leu
245	250		255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys	Tyr
260	265		270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu	Ala
275	280		285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp	Thr
290	295		300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu	Tyr
305	310		315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn	Ala
320	325		330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu	Glu
335	340		345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu	Ala
350	355		360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser	Val
365	370		375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile	Ser
380	385		390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val	Thr
395	400		405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg	Pro
410	415		420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly	Gly
425	430		435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser	Pro
440	445		450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met	Ile
455	460		465

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr  
470 475 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp  
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His  
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys  
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser  
530 535 540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens



<400> 122

gagatagggg gtctgggttt aagttcctgc tccatctcag gagcccctgc 50  
tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
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 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123  
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 35 40 45  
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
 50 55 60  
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
 65 70 75  
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
 80 85 90  
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
 95 100 105  
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
 110 115 120  
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
 125 130 135  
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
 140 145 150  
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
 155 160 165  
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly

	170	175	180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn			
	185	190	195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val			
	200	205	210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile			
	215	220	225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly			
	230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr			
	245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp			
	260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly			
	275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn			
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<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 124  
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<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 125  
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<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 126

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<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150

tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200

agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250

agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300

ggtgaacacc gtccctgaagc acatcatctg gctgaaggtc atcacagcta 350

acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400

gtcaagatcc cctcggacat ggtggctgga ttcaacacgc ccctggtcaa 450

gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500

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ccattcagct ctacctgggg gccaaagtgtg tggactcaca gggaaagggtg 850

accaagtggc tcaataactc tgcagcttcc ctgacaatgc ccacctgga 900

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cacctgggc atcgaagcca gctcgggaagc tcagttttac accaaagggtg 1250

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<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

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			20						25					30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35						40					45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
			50						55					60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
			65						70					75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
			80						85					90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
			95						100					105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
			110						115					120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
			125						130					135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
			140						145					150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
			155						160					165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu

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Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185					190					195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200					205					210
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
				215					220					225
Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys
				230					235					240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser
				245					250					255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu
				260					265					270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser
				275					280					285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu
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Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His
				305					310					315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp
				320					325					330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr
				335					340					345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu
				350					355					360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu
				365					370					375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr
				380					385					390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp
				395					400					405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp
				410					415					420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu
				425					430					435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu
				440					445					450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys

455	460	465
Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser		
470	475	480

Pro Val Ser Gln

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

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 aaagaaggag atggtgttat ctgaaaagg tagtcagctg atggaatgga 150  
 ctaacaaaag acctgtaata agaataaat gagacaagtt ccgtcgcctt 200  
 gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250  
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
 agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350  
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 aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaac 450  
 ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500  
 cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550  
 tagaccccc aattatgctg gtccccttat gttgggattg cttttggctg 600  
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 aataaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700  
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 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950  
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 aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

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20										25					30				
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met					
				35					40					45					
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys					
				50					55					60					
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile					
				65					70					75					
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys					
				80					85					90					
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg					
				95					100					105					
Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp					
				110					115					120					
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser					
				125					130					135					
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg					
				140					145					150					
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln					
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Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val					
				170					175					180					
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu					
				185					190					195					
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met					
				200					205					210					
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys					
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Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg					
				230					235					240					
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn					
				245					250					255					
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His					
				260					265					270					
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu					
				275					280					285					
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys					
				290					295					300					
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser					

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Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr					
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Ser Phe Leu Met Ser					
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<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
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 tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
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 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
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aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750  
ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800  
atgaaacagt ttaataaatt accaagtttt ggccgggcac agtggctcac 1850  
acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900  
aagagattga gaccatctg gccaacatgg tgaaacctg tctctactaa 1950  
aaatacaaaa attagctggg cgcggtgggtg cacacctata gtctcagcta 2000  
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agtgaactga gattgcgcca ctgtactcca gcctggcaac agagtgaagc 2100  
tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150  
tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200  
aatcacatat tttaaaaaat gggtattatt taggcctttg tacaatttct 2250  
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atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350  
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aaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala	
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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	
				20					25					30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	
				35					40					45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	
				50					55					60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	
				65					70					75	
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	

Tyr Ser Ser Tyr	Thr Lys Asn Cys Thr	Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn	Ile Arg Ala Phe Tyr	Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met	Leu Gly Glu Ile Ile	Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln	Lys Thr Ile Val Ile	Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met	Glu His Arg Gln Phe	Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala	His Val Pro Leu Leu	Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu	Gln Val Ser Asn Val	Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met	Leu Asp Ile Ala Gly	Ile Pro Leu Pro Gln Asn	365	370	375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	380	385	390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	395	400	405
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	410	415	420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	425	430	435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	440	445	450
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	455	460	465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	470	475	480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	485	490	495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	500	505	510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	515	520	525
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val	530	535	

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133  
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gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
ctacatccta ggcccttctgg ggcttttggg cacactgggt gccatgctgc 200  
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
gttggttctt ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
catcaccagc tgtgacatct atagcaccct tctgggcctg cccgctgaca 350  
tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctccctccctg 400  
gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450  
atccccgagc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500  
ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550  
ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600  
tgagagggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650  
ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700  
tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750  
gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
cagggtatgt gtgaagaacc aggggccaga gctggggggg ggctgggtct 850  
gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900  
actggatcgt gtcagaaggc gctgctgagg atagactgac tttggccatt 950  
ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000  
attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050  
gctcccttgc cctaagtccc caacctcaa cttgaaacct cattccctta 1100  
agccaggact cagaggatcc ctttgccctc tgggtttacct gggactccat 1150  
ccccaaacct actaatcaca tccactgac tgacctctg tgatcaaaga 1200  
ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250  
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300

cctccaaaga aactgattgg ccctggaacc tccatcccac tcttggtatg 1350  
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400  
 tacggtatcc agggacacaga aagcaggatg caggatggga ggacaggaag 1450  
 gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu	1	5	10	15
Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp	20	25	30	
Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly	35	40	45	
Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly	50	55	60	
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala	65	70	75	
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	80	85	90	
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr	95	100	105	
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala	110	115	120	
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro	125	130	135	
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro	140	145	150	
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	170	175	180	
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	185	190	195	
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	200	205	210	

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser  
 215 220 225

Leu Thr Gly Tyr Val  
 230

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 cttegctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100  
 aagtcacgcg tcccgtggc tcagaacct ggctgtgcca gccggcacc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200  
 cgccatcgtg tccctgagcg agaccgcca atgtgggtccc ccctgcacct 250  
 totggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaac 300  
 gattttgttg tgaagctgaa ggttcaggg gtgaattccc agtgccactc 350  
 atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggttttt caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu  
 1 5 10 15  
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys



	65		70		75									
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80						85					90
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
				95					100					105
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
				110					115					

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100  
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250  
 ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgcga ctacgcccgg acctcggatg acaggctttg tcgcagtgtc 350  
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450  
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
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 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggtgggga acccttcacc cttctgtgag attttccatc 700  
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<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys  
 1 5 10 15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20						25					30
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35						40					45
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50						55					60
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65						70					75
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80						85					90
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95						100					105
Cys	Arg	Ser	Val	Ser										
			110											

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
 cccaaggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
 tctcttcctg gctgcgtccc taggtccggt ggcagccttc aaggctcgcca 250  
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 tgcaggctct tgggccctgt ggacaaaggg cacgatgtga ccttctacaa 350  
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 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500  
 gtcggcctcc gaccacatg gcaacttctc catcaccatg cgcaacctga 550  
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 caccactcgg agcacagggt ccatgggtgcc atggagctgc aggtgcagac 650  
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 atacccgagg ccaaagtcag gcacccccctg tcctatgtgg cccagcggca 950  
 gccttctgag tctgggcggc atctgctttc ggagcccagc acccccctgt 1000  
 ctctccagg ccccgagagc gtcttcttcc catccctgga ccctgtccct 1050  
 gactctccaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggtt ggctctgtga 1150  
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 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
 atggggatgc tggacggctc agcccctgtt ccaaggattt tgggggtgctg 1300  
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450  
 tggggcaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500  
 ccccgaggcc gccttggctc ccccgttttg cccgaggctg ctcttctgtc 1550  
 agacttcctc tttgtaccac agtggctctg gggccaggcc tgcttgccta 1600  
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650  
 gatctgtcaa caggttaagt caatctgggg cttccactgc ctgcattcca 1700  
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750  
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800  
 gttgccccac ccactggaga tgggtgctgag ggaggtgggt ggggccttct 1850  
 ggggaaggtga gtggagaggg gcacctgcc cccgccctcc ccatccccta 1900  
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 ccacctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	
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Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	
				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp					
	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile					
	305		310		

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 cttagacctc ctttctgcc ctctttctct gccaccgct gcttctggc 150  
 ctttctccga ccccgctcta gcagcagacc tcttgggggc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250  
 ccgctcccg accagcggcc tgacctggg gaaaggatgg ttcccgaggt 300  
 gagggctctc tctctcttgc tgggactcgc gctgctctgg ttccccctgg 350  
 actcccacgc tcgagcccgc ccagacatgt tctgcctttt ccatgggaag 400  
 agatactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450  
 gatgtactgc ctgcgtgta cctgctcaga gggcgcccat gtgagttgtt 500  
 accgcctcca ctgtccgct gtccactgcc ccagcctgt gacggagcca 550  
 cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
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 agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700  
 gtctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
 cccgaacca ggtgcccag caccctccc actgccagac tctgctgcc 800  
 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
 cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900  
 tgggagaaag agaggcccgc gcacccagc cccactggc ctcagcgccc 950  
 ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000  
 actgtcaaga tcgtctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
 cgggaagacg tactccacg gggaggtgtg gcacccggcc ttccgtgct 1100

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 tgccagcgtg tgacctgtcc caccgagtag ccctgccgtc accccgagaa 1200  
 agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250  
 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
 ctggtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
 cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400  
 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
 ccacacagcc agaattttcc acttgactca gatcaagaaa gtcaggaagc 1500  
 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550  
 gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
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 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala
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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20					25					30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35					40					45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50					55					60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65					70					75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80					85					90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95					100					105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110					115					120

Gly Glu Ile Phe	Ser Ala His Glu Leu	Phe Pro Ser Arg Leu	Pro
125		130	135
Asn Gln Cys Val	Leu Cys Ser Cys Thr	Glu Gly Gln Ile Tyr	Cys
140		145	150
Gly Leu Thr Thr	Cys Pro Glu Pro Gly	Cys Pro Ala Pro Leu	Pro
155		160	165
Leu Pro Asp Ser	Cys Cys Gln Ala Cys	Lys Asp Glu Ala Ser	Glu
170		175	180
Gln Ser Asp Glu	Glu Asp Ser Val Gln	Ser Leu His Gly Val	Arg
185		190	195
His Pro Gln Asp	Pro Cys Ser Ser Asp	Ala Gly Arg Lys Arg	Gly
200		205	210
Pro Gly Thr Pro	Ala Pro Thr Gly Leu	Ser Ala Pro Leu Ser	Phe
215		220	225
Ile Pro Arg His	Phe Arg Pro Lys Gly	Ala Gly Ser Thr Thr	Val
230		235	240
Lys Ile Val Leu	Lys Glu Lys His Lys	Lys Ala Cys Val His	Gly
245		250	255
Gly Lys Thr Tyr	Ser His Gly Glu Val	Trp His Pro Ala Phe	Arg
260		265	270
Ala Phe Gly Pro	Leu Pro Cys Ile Leu	Cys Thr Cys Glu Asp	Gly
275		280	285
Arg Gln Asp Cys	Gln Arg Val Thr Cys	Pro Thr Glu Tyr Pro	Cys
290		295	300
Arg His Pro Glu	Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys	Pro
305		310	315
Glu Asp Lys Ala	Asp Pro Gly His Ser	Glu Ile Ser Ser Thr	Arg
320		325	330
Cys Pro Lys Ala	Pro Gly Arg Val Leu	Val His Thr Ser Val	Ser
335		340	345
Pro Ser Pro Asp	Asn Leu Arg Arg Phe	Ala Leu Glu His Glu	Ala
350		355	360
Ser Asp Leu Val	Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp	Glu
365		370	375
Glu Thr Glu Ala	Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro	His
380		385	390
Ser Gln Asn Leu	Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu	Ala
395		400	405

Arg	Leu	Pro	Glu	Arg	Gly	Thr	Ala	Leu	Pro	Thr	Ala	Arg	Trp	Pro
			410						415					420
Pro	Arg	Arg	Ser	Leu	Glu	Arg	Leu	Pro	Ser	Pro	Asp	Pro	Gly	Ala
			425						430					435
Glu	Gly	His	Gly	Gln	Ser	Arg	Gln	Ser	Asp	Gln	Asp	Ile	Thr	Lys
			440						445					450

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gtcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgcctcc gtgggcgccc 400  
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450  
 ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500  
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 tttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
 1 5 10 15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30



Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90
Arg	Ser	Pro												

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100  
 caggctgcca tggggcccag caccctctc ctcatcttgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttgtg gagtacatgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtcttg agcgggaggt agactatctg 400  
 gagaccaga acccagctct gccctgtgta gaggttgatg agaaggtgac 450  
 tggaggccct gggaccaaag gcaagggaa aaggaatgag aagtacgata 500  
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600  
 gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650  
 ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700  
 gcttcccag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750  
 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800  
 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
 aaccgaacag tgggtggacag ctgagtattc ccagcagagg ggctgatccc 900

cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
 aagggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000  
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
 accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100  
 tctatgtcgt ctataacacc cgtcctgcca gtcgggcccg catccagtgc 1150  
 tcctttgatg ccagcggcac cctgaccctt gaacgggcag cactccctta 1200  
 ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250  
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
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 cccagacca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650  
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 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn

	50		55		60
Lys Met Leu Pro Leu Leu Glu Val Ala	65	Glu Lys Glu Arg Glu Ala	70		75
Leu Arg Thr Glu Ala Asp Thr Ile Ser	80	Gly Arg Val Asp Arg Leu	85		90
Glu Arg Glu Val Asp Tyr Leu Glu Thr	95	Gln Asn Pro Ala Leu Pro	100		105
Cys Val Glu Phe Asp Glu Lys Val Thr	110	Gly Gly Pro Gly Thr Lys	115		120
Gly Lys Gly Arg Arg Asn Glu Lys Tyr	125	Asp Met Val Thr Asp Cys	130		135
Gly Tyr Thr Ile Ser Gln Val Arg Ser	140	Met Lys Ile Leu Lys Arg	145		150
Phe Gly Gly Pro Ala Gly Leu Trp Thr	155	Lys Asp Pro Leu Gly Gln	160		165
Thr Glu Lys Ile Tyr Val Leu Asp Gly	170	Thr Gln Asn Asp Thr Ala	175		180
Phe Val Phe Pro Arg Leu Arg Asp Phe	185	Thr Leu Ala Met Ala Ala	190		195
Arg Lys Ala Ser Arg Val Arg Val Pro	200	Phe Pro Trp Val Gly Thr	205		210
Gly Gln Leu Val Tyr Gly Gly Phe Leu	215	Tyr Phe Ala Arg Arg Pro	220		225
Pro Gly Arg Pro Gly Gly Gly Gly Glu	230	Met Glu Asn Thr Leu Gln	235		240
Leu Ile Lys Phe His Leu Ala Asn Arg	245	Thr Val Val Asp Ser Ser	250		255
Val Phe Pro Ala Glu Gly Leu Ile Pro	260	Pro Tyr Gly Leu Thr Ala	265		270
Asp Thr Tyr Ile Asp Leu Val Ala Asp	275	Glu Glu Gly Leu Trp Ala	280		285
Val Tyr Ala Thr Arg Glu Asp Asp Arg	290	His Leu Cys Leu Ala Lys	295		300
Leu Asp Pro Gln Thr Leu Asp Thr Glu	305	Gln Gln Trp Asp Thr Pro	310		315
Cys Pro Arg Glu Asn Ala Glu Ala Ala	320	Phe Val Ile Cys Gly Thr	325		330
Leu Tyr Val Val Tyr Asn Thr Arg Pro		Ala Ser Arg Ala Arg Ile			

	335		340		345
Gln Cys Ser Phe	Asp Ala Ser Gly Thr	Leu Thr Pro Glu Arg	Ala		
	350		355		360
Ala Leu Pro Tyr	Phe Pro Arg Arg Tyr	Gly Ala His Ala Ser	Leu		
	365		370		375
Arg Tyr Asn Pro	Arg Glu Arg Gln Leu	Tyr Ala Trp Asp Asp	Gly		
	380		385		390
Tyr Gln Ile Val	Tyr Lys Leu Glu Met	Arg Lys Lys Glu Glu	Glu		
	395		400		405

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
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 gttctctct tctctctaata ccatccgtca cctctctctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250  
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctct 300  
 gtttctctgt tcttaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500  
 ttggatgctg gcctctatgg gtgcaggatt agttcccagt ctactacca 550  
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600  
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650  
 tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700  
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750  
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800  
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850

aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
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 gagatttaca aggaagagtg tggtggcttc tcagagtttc caagcagggg 1200  
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 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
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 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700  
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 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950  
 tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
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aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

1	5	10	15
Ser Gly Gln Trp	Gln Val Phe Gly Pro	Asp Lys Pro Val	Gln Ala
	20	25	30
Leu Val Gly Glu	Asp Ala Ala Phe Ser	Cys Phe Leu Ser	Pro Lys
	35	40	45
Thr Asn Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Gly	Gln Phe
	50	55	60
Ser Ser Val Val	His Leu Tyr Arg Asp	Gly Lys Asp Gln	Pro Phe
	65	70	75
Met Gln Met Pro	Gln Tyr Gln Gly Arg	Thr Lys Leu Val	Lys Asp
	80	85	90
Ser Ile Ala Glu	Gly Arg Ile Ser Leu	Arg Leu Glu Asn	Ile Thr
	95	100	105
Val Leu Asp Ala	Gly Leu Tyr Gly Cys	Arg Ile Ser Ser	Gln Ser
	110	115	120
Tyr Tyr Gln Lys	Ala Ile Trp Glu Leu	Gln Val Ser Ala	Leu Gly
	125	130	135
Ser Val Pro Leu	Ile Ser Ile Thr Gly	Tyr Val Asp Arg	Asp Ile
	140	145	150
Gln Leu Leu Cys	Gln Ser Ser Gly Trp	Phe Pro Arg Pro	Thr Ala
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Thr Asp	Ser Arg
	170	175	180
Thr Asn Arg Asp	Met His Gly Leu Phe	Asp Val Glu Ile	Ser Leu
	185	190	195
Thr Val Gln Glu	Asn Ala Gly Ser Ile	Ser Cys Ser Met	Arg His
	200	205	210
Ala His Leu Ser	Arg Glu Val Glu Ser	Arg Val Gln Ile	Gly Asp
	215	220	225
Thr Phe Phe Glu	Pro Ile Ser Trp His	Leu Ala Thr Lys	Val Leu
	230	235	240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly	Leu Lys
	245	250	255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu	Leu Asp
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala	Arg Lys
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His	Pro Lys

290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 151  
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
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aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggag 150  
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200  
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caccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
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gaaacctgca aagagggcctt ttacctaaat tacacttctg ggctctgtca 850  
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taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450  
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500  
tatctaagca ttgacctgt actgcactga aagtaattat tctttgacct 1550  
tatgtgaggc acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600  
acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650  
tggttataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700  
agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750  
taaagaggt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800  
ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850  
tgttttaaga acttttagct ccttgacaaa gaagtgttt atacttttagc 1900  
actaaatatt ttaaagctt tataaatgat attatactgt tatggaatat 1950  
tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000  
ctcacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050  
tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgct 2100  
ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150  
tcccagctac tcgggagggt gaggcaggag aatcggttga acccgggagg 2200

tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250

agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10					15

Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30

Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45

Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60

Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75

Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90

Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105

Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120

Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135

Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150

Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165

Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180

Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195

Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210

Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225

Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys	Gln	Pro	Cys	Asp	Cys	Ser	Pro	His	Gly	Ala	Leu	Ser	Ile	Pro
				245					250					255

Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 154

aactgctctg tggttggaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 155

cagtcacatg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 156

aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157

<211> 689

<212> DNA

<213> Homo sapiens

<400> 157

tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50

ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100

ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150

ccgggaaaag ggctttgcc aaggagaagga catgaagaac gtcgtggggg 200

tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250

cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
tgctggccac caacttcaga gactatgcca tcattctcac tcagctggag 400  
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500  
gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600  
gggtcctgtg acctcggccca gtgtccaccc acctcgctca gcggctcccg 650  
gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158

<211> 163

<212> PRT

<213> Homo sapiens

<400> 158

Met	Gly	Gly	Leu	Leu	Leu	Ala	Ala	Phe	Leu	Ala	Leu	Val	Ser	Val
1				5					10					15
Pro	Arg	Ala	Gln	Ala	Val	Trp	Leu	Gly	Arg	Leu	Asp	Pro	Glu	Gln
				20					25					30
Leu	Leu	Gly	Pro	Trp	Tyr	Val	Leu	Ala	Val	Ala	Ser	Arg	Glu	Lys
				35					40					45
Gly	Phe	Ala	Met	Glu	Lys	Asp	Met	Lys	Asn	Val	Val	Gly	Val	Val
				50					55					60
Val	Thr	Leu	Thr	Pro	Glu	Asn	Asn	Leu	Arg	Thr	Leu	Ser	Ser	Gln
				65					70					75
His	Gly	Leu	Gly	Gly	Cys	Asp	Gln	Ser	Val	Met	Asp	Leu	Ile	Lys
				80					85					90
Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159

<211> 1665  
<212> DNA  
<213> Homo sapiens

<400> 159  
aacagacgtt ccctgcggc cctggcacct ctaaccccag acatgctgct 50  
gctgctgctg cccctgctct gggggagggg gagggcgga ggacagacaa 100  
gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150  
gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggattttacc 200  
tggcccagta gttcatggct actgggtccg ggaaggggcc aatacagacc 250  
aggatgctcc agtggccaca aacaacccag ctggggcagt gtgggaggag 300  
actggggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400  
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600  
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcaccccaca 650  
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700  
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750  
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850  
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900  
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950  
gggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050  
ctgcagagca aagccacatc aggagtgact caggggggtg tcgggggagc 1100  
tggagccaca gccctggctt tcctgtcctt ctgcgtcatc ttcggtgtag 1150  
tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctacggggcc 1250  
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

cttctgccccg ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350  
 agcttccaga tggatgaagcc ttgggactcg cggggacagg aggccactga 1400  
 caccgagtagc tcggagatca agatccacag atgagaaaact gcagagactc 1450  
 accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550  
 atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600  
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160  
 <211> 463  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala  
 1 5 10 15  
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr  
 20 25 30  
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr  
 35 40 45  
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr  
 50 55 60  
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala  
 65 70 75  
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg  
 80 85 90  
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser  
 95 100 105  
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg  
 110 115 120  
 Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu  
 125 130 135  
 Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile  
 140 145 150  
 Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser  
 155 160 165  
 Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp  
 170 175 180

Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg	Ser
	185	190	195
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr	Ser
	200	205	210
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr	Asn
	215	220	225
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu Thr	
	230	235	240
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu Gly	
	245	250	255
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg	Leu
	260	265	270
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg	Leu
	275	280	285
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro	Ser
	290	295	300
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp	Ala
	305	310	315
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln	Gln
	320	325	330
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly	Val
	335	340	345
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val	Phe
	350	355	360
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg	Lys
	365	370	375
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile	Glu
	380	385	390
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu	Thr
	395	400	405
Glu Pro Trp Ala	Glu Asp Ser Pro Pro	Asp Gln Pro Pro Pro	Ala
	410	415	420
Ser Ala Arg Ser	Ser Val Gly Glu Gly	Glu Leu Gln Tyr Ala	Ser
	425	430	435
Leu Ser Phe Gln	Met Val Lys Pro Trp	Asp Ser Arg Gly Gln	Glu
	440	445	450
Ala Thr Asp Thr	Glu Tyr Ser Glu Ile	Lys Ile His Arg	
	455	460	

<210> 161  
<211> 739  
<212> DNA  
<213> Homo sapiens

<400> 161  
gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100  
cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200  
aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250  
gagggaggat cgggtgatcc agaagaaaat cctgatgcgg aagacggagg 300  
agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400  
tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500  
tcggaggagg acattttcac gcccctgcag acgggaagct gcgttccccga 550  
aactaggca gcccccggt ctgcacctcc agagcccacc ctaccaccag 600  
acacagagcc cggaccacct ggacctacc tccagccatg acccttccct 650  
gtcccccacc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
<211> 170  
<212> PRT  
<213> Homo sapiens

<400> 162  
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
1 5 10 15  
Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr  
20 25 30  
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg  
35 40 45  
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly  
50 55 60  
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile  
65 70 75



Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr  
80 85 90

Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro  
95 100 105

Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly  
110 115 120

Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr  
125 130 135

Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys  
140 145 150

Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser  
155 160 165

Cys Val Pro Glu His  
170

<210> 163  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 163  
ggagatgaag accctgttcc tg 22

<210> 164  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 164  
ggagatgaag accctgttcc tgggtg 26

<210> 165  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 165  
gtcctccgga aagtccttat c 21

<210> 166  
<211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
gcctagtgtt cggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 168  
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169  
gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50  
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150  
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200  
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtggg 250  
cgacgtcat cgccccaga tggctcctga cagcagcca ctgcctcaag 300  
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggagg 350  
ctgtgagcag acccggacag ccaactgagtc cttccccac cccggcttca 400  
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500

ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550  
 gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600  
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650  
 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
 gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750  
 attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctgggtgt 800  
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850  
 acaattagac tggaccacc caccacagcc catcaccctc catttccact 900  
 tgggtgtttgg ttctgttca ctctgtta atagaaaccct aagccaagac 950  
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000  
 taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050  
 ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100  
 tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150  
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaa 1204

<210> 170  
 <211> 250  
 <212> PRT  
 <213> Homo sapiens

<400> 170  
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
 1 5 10 15  
 Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro  
 20 25 30  
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu  
 35 40 45  
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala  
 50 55 60  
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His  
 65 70 75  
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr  
 80 85 90  
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys  
 95 100 105

Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

ggctgcgga ctggaagtca tcggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 173  
cctctgtgtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 175  
cgtgtagaca ccaggctttc gggcg 25

<210> 176  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 176  
cccttgatga tcctgggc 18

<210> 177  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 177  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 178  
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179  
<211> 907  
<212> DNA  
<213> Homo sapiens

<400> 179  
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50  
gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100  
aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150  
agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200  
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250  
caaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300  
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350  
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400  
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<211> 222  
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Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	155	160	165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	170	175	180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	200	205	210
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<213> Artificial Sequence

<220>

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cc 52

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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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				20					25					30

Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
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Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
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Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu
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<210> 192  
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<212> DNA  
<213> Homo sapiens

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<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

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Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu
				35					40					45
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala
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Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly
				80					85					90
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His
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Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val
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Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	
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Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	
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Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	
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Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	
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Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	
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Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	
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Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	
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<211> 1485

<212> DNA

<213> Homo sapiens

<400> 195

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 35 40 45  
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp  
 50 55 60  
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met  
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Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys  
80 85 90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr  
95 100 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu  
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 gttgggacag ccatgtggga cccctggtg attcagcatg aaggaaatga 4750  
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 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg
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Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro
			20					25					30	

Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45				
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro
				50					55					60
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg
				65					70					75
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu
				80					85					90
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe
				95					100					105
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys
				110					115					120
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu
				125					130					135
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg
				140					145					150
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp
				155					160					165
Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu
				170					175					180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Ile	Ser	Arg	
				185					190					195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu
				200					205					210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp
				215					220					225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr
				230					235					240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp
				245					250					255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro
				260					265					270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr
				275					280					285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu
				290					295					300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu
				305					310					315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr

320					325					330				
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp
				335					340					345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu
				350					355					360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe
				365					370					375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys
				380					385					390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu
				395					400					405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys
				410					415					420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala
				425					430					435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp
				440					445					450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser
				455					460					465
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser
				470					475					480
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe
				485					490					495
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
				500					505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
				515					520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
				530					535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
				545					550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys
				560					565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu
				575					580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val
				590					595					600
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn

605					610					615				
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
				620					625					630
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
				650					655					660
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
				665					670					675
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
				680					685					690
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
				710					715					720
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750
Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr
				755					760					765
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile
				770					775					780
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe
				785					790					795
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg
				800					805					810
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu
				815					820					825
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu
				830					835					840
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly
				845					850					855
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu
				860					865					870
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser
				875					880					885
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr

890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly Thr	
920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro Tyr	
935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys Ile	
950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr	Cys His Leu Ser Asp Ser	
965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu Gly	
980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp Cys	
995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val Cys	
1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val Ile	
1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu	Cys Gln His Glu Ala Lys	
1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser	Cys Glu Cys Val Pro Gly	
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp	Asn Asp Asp Cys Val Ala	
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys	Val Asp Thr Ile Asn Gly	
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe	Ser Gly Pro Phe Cys Glu	
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln	Thr Ser Pro Cys Asp Gln	
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys	Ile Val Val Gln Gln Glu	
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe	Ala Gly Pro Arg Cys Glu	
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly	Lys Asp Ser Tyr Val Glu	
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln	Ala Asn Ile Ser Leu Gln	

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp 1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu 1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val 1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr 1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys 1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser 1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala 1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys 1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala 1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys 1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser 1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp 1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly 1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu 1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn 1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser 1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly 1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg 1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
1520		

<210> 199  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 199  
 atggagattc ctgccaaactt gccg 24

<210> 200  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 200  
 ttgttggcat tgaggaggag cagc 24

<210> 201  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 201  
 gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
 <211> 753  
 <212> DNA  
 <213> Homo sapiens

<400> 202  
 ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
 gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150  
 cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
 atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
 caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
 agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
 gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400  
 gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
 atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
 caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
 cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600  
 ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
 cctgtgtcat cttgtcccggt ttcctcccaa tattccttct caaacttgga 700  
 gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750  
 gtc 753

<210> 203

<211> 148

<212> PRT

<213> Homo sapiens

<400> 203

Met	Lys	Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr
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Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
				110					115					120



Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
140 145

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

gcaggctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

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<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

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tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250  
agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350  
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
ctgatgtcct ctatccatct ctaaatgtca ccagctttga ctcagttgtt 450  
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500  
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcaactggaag 550  
ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggtt 600  
catctgatcg tggcaggtgg ttatgacgag agagtccctgg agaattgtga 650  
acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
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cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
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cggttggaacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
gagcctgacc cggtgcactt ctgagaagca atagaaaagt tcatccgtga 950  
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aaaaattttc ccctgaagca ttacagAAC agctctaccg atatgttacc 1050  
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ttatggattg tagaccaggt tttgaaacca aaaaagaaac ctagaatcta 1150

atgcagaaga gatcttttaa aaaataaaact tgagtcttga atgtgagcca 1200  
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
 tttatgctat aatcattcca aattttgccca gtgttaagtt acaaagtgg 1300  
 tgtcattcca tgttcagcag agtatatttaa ttatattttc tcgggattat 1350  
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
 atagttaaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450  
 ataatgagag cagggtatt gtagttccca gattcaatcc accgaagtgt 1500  
 tcaactgtcat ctgttaggga atttttgttt gtcctgtctt tgcctggatc 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaa 1648

<210> 210  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 210  
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 Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val  
 20 25 30  
 Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His  
 35 40 45  
 Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg  
 50 55 60  
 Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly  
 65 70 75  
 Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val  
 80 85 90  
 Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val  
 95 100 105  
 Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro  
 110 115 120  
 Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu  
 125 130 135  
 Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala  
 140 145 150  
 Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp

	155	160	165
Trp Glu Arg Val	His Leu Ile Val Ala	Gly Gly Tyr Asp Glu	Arg
	170	175	180
Val Leu Glu Asn	Val Glu His Tyr Gln	Glu Leu Lys Lys Met	Val
	185	190	195
Gln Gln Ser Asp	Leu Gly Gln Tyr Val	Thr Phe Leu Arg Ser	Phe
	200	205	210
Ser Asp Lys Gln	Lys Ile Ser Leu Leu	His Ser Cys Thr Cys	Val
	215	220	225
Leu Tyr Thr Pro	Ser Asn Glu His Phe	Gly Ile Val Pro Leu	Glu
	230	235	240
Ala Met Tyr Met	Gln Cys Pro Val Ile	Ala Val Asn Ser Gly	Gly
	245	250	255
Pro Leu Glu Ser	Ile Asp His Ser Val	Thr Gly Phe Leu Cys	Glu
	260	265	270
Pro Asp Pro Val	His Phe Ser Glu Ala	Ile Glu Lys Phe Ile	Arg
	275	280	285
Glu Pro Ser Leu	Lys Ala Thr Met Gly	Leu Ala Gly Arg Ala	Arg
	290	295	300
Val Lys Glu Lys	Phe Ser Pro Glu Ala	Phe Thr Glu Gln Leu	Tyr
	305	310	315
Arg Tyr Val Thr	Lys Leu Leu Val		
	320		

<210> 211  
 <211> 1554  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
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 cttcgcgata ttgcgcgtta cttctttgct ggcgttggtg ggagccgtgc 100  
 tctaccteta tccggcttcc agacaagctg caggaattcc agggattact 150  
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200  
 tttgcatgag ttcttggtta atttgcatga gagatatggg cctgtggtct 250  
 ccttctgggtt tggcaggcgc ctctgtggtta gtttgggcac tgttgatgta 300  
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000  
 ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150  
 tgggtacttca ggatcctaact acttggccat ctccacacaa gtttgatcca 1200  
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250  
 ctcaggcaca caggagtgtc cagagttgag gtttgcataat atggtgacca 1300  
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1					5				10					15

Val Gly Ala Val	Leu Tyr Leu Tyr	Pro Ala Ser Arg	Gln Ala Ala	
	20	25	30	
Gly Ile Pro Gly	Ile Thr Pro Thr	Glu Glu Lys Asp	Gly Asn Leu	
	35	40	45	
Pro Asp Ile Val	Asn Ser Gly Ser	Leu His Glu Phe	Leu Val Asn	
	50	55	60	
Leu His Glu Arg	Tyr Gly Pro Val	Val Ser Phe Trp	Phe Gly Arg	
	65	70	75	
Arg Leu Val Val	Ser Leu Gly Thr	Val Asp Val Leu	Lys Gln His	
	80	85	90	
Ile Asn Pro Asn	Lys Thr Ser Asp	Pro Phe Glu Thr	Met Leu Lys	
	95	100	105	
Ser Leu Leu Arg	Tyr Gln Ser Gly	Gly Gly Ser Val	Ser Glu Asn	
	110	115	120	
His Met Arg Lys	Lys Leu Tyr Glu	Asn Gly Val Thr	Asp Ser Leu	
	125	130	135	
Lys Ser Asn Phe	Ala Leu Leu Leu	Lys Leu Ser Glu	Glu Leu Leu	
	140	145	150	
Asp Lys Trp Leu	Ser Tyr Pro Glu	Thr Gln His Val	Pro Leu Ser	
	155	160	165	
Gln His Met Leu	Gly Phe Ala Met	Lys Ser Val Thr	Gln Met Val	
	170	175	180	
Met Gly Ser Thr	Phe Glu Asp Asp	Gln Glu Val Ile	Arg Phe Gln	
	185	190	195	
Lys Asn His Gly	Thr Val Trp Ser	Glu Ile Gly Lys	Gly Phe Leu	
	200	205	210	
Asp Gly Ser Leu	Asp Lys Asn Met	Thr Arg Lys Lys	Gln Tyr Glu	
	215	220	225	
Asp Ala Leu Met	Gln Leu Glu Ser	Val Leu Arg Asn	Ile Ile Lys	
	230	235	240	
Glu Arg Lys Gly	Arg Asn Phe Ser	Gln His Ile Phe	Ile Asp Ser	
	245	250	255	
Leu Val Gln Gly	Asn Leu Asn Asp	Gln Gln Ile Leu	Glu Asp Ser	
	260	265	270	
Met Ile Phe Ser	Leu Ala Ser Cys	Ile Ile Thr Ala	Lys Leu Cys	
	275	280	285	
Thr Trp Ala Ile	Cys Phe Leu Thr	Thr Ser Glu Glu	Val Gln Lys	
	290	295	300	

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
				305					310					315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320					325					330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335					340					345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350					355					360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365					370					375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380					385					390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395					400					405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410					415					420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425					430					435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440					445					450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455					460						

<210> 213  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
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 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100  
 tcagggttg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150  
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
 ctctcacgtt caccoccgag gaggatgaca agcaggacat tcagctggtg 250  
 gccgcgtct ctgtaccct gggcctcttt gcagtggagc tggccggttt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400  
 tgggagtgca ctacgtattg gtacatTTTT gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggtt 600  
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
 tgttttgtag taacattaag acttatatac agttttaggg gacaattaa 750  
 aaaaaaaaaa 759

<210> 214  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 214  
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
 1 5 10 15  
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
 20 25 30  
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
 35 40 45  
 Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
 50 55 60  
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
 65 70 75  
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
 80 85 90  
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
 95 100 105  
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
 110 115 120  
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
 125 130 135  
 Lys Lys Lys Pro Phe  
 140

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccggaccc tgccgccttg ccactatgtc ccgccgctct atgctgcttg 50



cctgggctct ccccgacctc cttcgactcg gagcggctca ggagacagaa 100  
gacccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150  
ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
tatcgcacac ggcgggcagc agctgcaaca ccccgacctc gtgccagcag 250  
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
gtggctggaa ctacagggg gcccactcag gtcacttatg gaaccccatg 400  
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450  
ccaggccatc cgggcagccc aggggtctact ggcctgcggt gtggctcagg 500  
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
ctaccgtcc cctgagggcc ctgctgatcc gcacccatt cctcccctcc 650  
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1				5					10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
			20						25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
			35						40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
			50						55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
			65						70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
			80						85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
			95						100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
			110						115					120

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
			125						130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
			140						145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
			155						160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
			170						175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
			185						190					195

Pro

<210> 217  
 <211> 1871  
 <212> DNA  
 <213> Homo sapiens

<400> 217  
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 gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100  
 tctatctggt catctgtggc caggatgatg gtcctcccgg ctgagaggac 150  
 cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcggaa 200  
 gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250  
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300  
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350  
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400  
 tgctcgtcac aggaagatt gtggaccatg gcaatgggac cttcagcgtc 450  
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500  
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550  
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600  
 gaacggggcc gccggacctc gctttgcacc cacgaccag ccaagatctg 650  
 ctcccagagac cacgctcaga gtcagccac ctggagctgc tcccagccct 700  
 tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggtg 750  
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800  
 cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850

ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900  
 gttgggcctc aggcaggagag ggggggtggag acgaggagat gccaagtggg 950  
 gccagggccca agtctcaagt ggcagagaaa gggtoccaag tgctgggtccc 1000  
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050  
 ggtctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100  
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150  
 gtcattgggag gaagctaagc ccttggttct tgccatctg aggaaagata 1200  
 gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250  
 atggatggct gagagggtct cctaggagcc agtcagcagg gtgggggtggg 1300  
 gccagaggag ctctccagcc ctgcctagtg ggcgcctga gcccttctc 1350  
 gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400  
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450  
 ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500  
 cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc 1550  
 acagcccatc cgcgtgctgt gtgtccctct tccaccccaa cccctgctgg 1600  
 ctctcttggg agcatccatg tcccggagag gggtcctca acagtcagcc 1650  
 tcacctgtca gaccgggggt ctcccggatc tggatggcgc cgccctctca 1700  
 gcagcgggca cgggtggggc ggggcccggc cgcagagcat gtgctggatc 1750  
 tgttctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800  
 aaccgtgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850  
 aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
1					5				10					15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20					25					30
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	
				50					55					60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	
				65					70					75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	
				80					85					90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	
				95					100					105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	
				110					115					120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	
				125					130					135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	
				140					145					150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	
				155					160					165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	
				170					175					180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	
				185					190					195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	
				200					205					210	
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	
				215					220					225	
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	
				230					235					240	
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				
				245					250						

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150

agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200

gcgccgccgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250  
tcttcccagag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300  
agcgccagcc ggctgcggct gccacacgg ctcaccatgg gctccgggcg 350  
ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400  
ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggtc 500  
ctcttctctc ccgctgggga tatcggtccg ggcggccaac tccaaggctc 550  
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600  
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650  
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700  
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750  
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800  
tgttactcgt gaagctgcca cgaatggtgt cctgctctac ctagataaaag 850  
aggataaggt ttacctaaaa ctggagaaaag gtaatttggt tggaggctgg 900  
cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950  
ttctccatga tgttcatcca ggtgagggat gacccactcc tgagttattg 1000  
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
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tcacagatta ttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150  
aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200  
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250  
gaattttatt tgtttagttt taaaagactg gcaaccaggt ctaaggatta 1300  
gaaaactcta aagtctgac ttcaatcaac ggtagtggtg atactgccaa 1350  
agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400  
ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450  
aactgggtatt atgttttctc ttaaaataag gtaatgaatg gcttgccac 1500  
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550  
gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600  
ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

aaagttgctt acccaaaatc taagtgtc atccctgagc ctcagcaaaa 1700  
 cagctccccct ccgagggaaa tcttatactt tattgtc ttttaattaa 1750  
 aatgattgat aataaccact ttattaaaaa cctaagggtt tttttttttc 1800  
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850  
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900  
 tgccttaact ctttaaattg tatataattt tctgttttagc taatattaaa 1950  
 ttcaaataat ccatatctaa atttagtgca atatcttgtc ttttgtatag 2000  
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050  
 tatatgttaa aaaaa 2065

<210> 220  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 220  
 Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu  
 1 5 10 15  
 Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp  
 20 25 30  
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp  
 35 40 45  
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu  
 50 55 60  
 Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala  
 65 70 75  
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr  
 80 85 90  
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe  
 95 100 105  
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr  
 110 115 120  
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile  
 125 130 135  
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe  
 140 145 150  
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val  
 155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
185 190 195

Phe Leu Val Phe Pro Leu  
200

<210> 221

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 221

acggctcacc atgggctccg 20

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

aggaagagga gcccttggag tccg 24

<210> 223

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224

<211> 902

<212> DNA

<213> Homo sapiens

<400> 224

cggtggccat gactgcggcc gtgtttcttcg gctgcgcctt cattgccttc 50

gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100

tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150

tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200

ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
 tatccaagaa atgttccgat ttgcatatta taaactotta aaaaaagcca 300  
 gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350  
 ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400  
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<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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Ala	Leu	Pro	Lys	Ala	Gln	Pro	Ala	Glu	Leu	Ser	Val	Glu	Val	Pro
				20					25					30
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
				35					40					45
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
				50					55					60
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala

80										85					90				
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					
Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn					
				320					325					330					
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile					
				335					340					345					
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala					
				350					355					360					
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr					

365					370					375				
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala
				380					385					390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu
				395					400					405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met
				410					415					420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val
				425					430					435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile
				440					445					450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro
				455					460					465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu
				470					475					480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr
				485					490					495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val
				500					505					510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser
				515					520					525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly
				530					535					540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val
				545					550					555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu
				560					565					570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr
				575					580					585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu
				590					595					600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly
				605					610					615
Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp
				620					625					630
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu
				635					640					645
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His

650					655					660				
Gly	Leu	Ile	Val	Ser	Gly	Pro	Ser	Lys	Asp	Pro	Asp	Leu	Ala	Ser
				665					670					675
Gly	His	Gly	Pro	Tyr	Ser	Phe	Thr	Leu	Gly	Pro	Asn	Pro	Thr	Val
				680					685					690
Gln	Arg	Asp	Trp	Arg	Leu	Gln	Thr	Leu	Asn	Gly	Ser	His	Ala	Tyr
				695					700					705
Leu	Thr	Leu	Ala	Leu	His	Trp	Val	Glu	Pro	Arg	Glu	His	Ile	Ile
				710					715					720
Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val
				725					730					735
Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg
				740					745					750
Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val
				755					760					765
Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile
				770					775					780
Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp
				785					790					795
Gln	Pro	Ala	Asp	Ser	Val	Pro	Leu	Lys	Ala	Thr	Val			
				800					805					

<210> 230

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

cgccttaccg cgcagcccca agattcacta tggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

cctgagctgt aaccccactc cagg 24

<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50  
atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100  
cagaaatgga gacgagatca gcaaatgag tcaactagtg aattcaaaca 150  
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
gatgtcctgg tcccatctgt cagtctgcag gcatttaaatt ccttcctgag 250  
atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300  
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350  
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400  
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450  
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500  
actgggaaag gcgtgaggcg gccggccgtt tggtgaatg caggcatcca 550  
ttcccagagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600  
ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650  
atggatatatt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700  
tcaaactcaa aaccgattat ggaggaagac gcggtcccg aatcctggaa 750  
gctcctgcat tgggtgtgac ccaaatagaa actggaacgc tagttttgca 800  
ggaaaggggag ccagcgacaa cccttgtctc gaagtgtacc atggacccca 850  
cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900  
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atgtatccat atgggtactc agtcaaaaag gccccagatg ccgaggaact 1000  
cgacaagggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050  
ctgagtacca agtgggtccc acctgcacca ctgtctatcc agctagcggg 1100

agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150  
tgagttgaga gataccggga cctatggctt cctcctgcca gctaaccaga 1200  
tcatccccac tgcagaggag acgtggctgg ggctgaagac catcatggag 1250  
catgtgcggg acaacctcta ctaggcgatg gctctgctct gtctacattt 1300  
atttgtaccc acacgtgcac gcactgaggc cattgttaaa ggagctcttt 1350  
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agccactgtg ccgggcccgt cccctccttt tttaggcctg aatacaaagt 2150  
agaagatcac tttccttcac tgtgctgaga atttctagat actacagttc 2200  
ttactcctct cttccctttg ttattcagtg tgaccaggat ggcgggaggg 2250  
gatctgtgtc actgtaggta ctgtgccag gaaggctggg tgaagtgacc 2300  
atctaaattg caggatgggt aaattatccc catctgtcct aatgggctta 2350  
cctcctcttt gccttttgaa ctcaactcaa agatctaggc ctcatcttac 2400  
aggtcctaaa tcaactcatc ggccctggata atctcactgc cctggcacat 2450  
tcccatttgt gctgtgggtg atcctgtgtt tccttgcctt ggtttgtgtg 2500

tgtgtgtgtg tgtgtgtgtg tgtgtgtgtt tgtgtgtgtg tgtctgtcta 2550  
 ttttgtatcc tggaccacaa gttcctaagt agagcaagaa ttcatcaacc 2600  
 agctgcctct tgtttcattt cacctcagca cgtaccatct gtccttttgt 2650  
 tgttgttgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700  
 tcttaacctc ctgcctagga tttgtacagc atctggtgtg tgcttataag 2750  
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile	1	5	10	15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn	20	25	30	
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn	35	40	45	
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala	65	70	75	
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr	80	85	90	
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met	95	100	105	
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr	110	115	120	
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn	125	130	135	
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly	140	145	150	
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr	155	160	165	
Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195	

Arg Lys Ile Val	Ser Asp Tyr Gln Arg	Asp Pro Ala Ile Thr	Ser
	200	205	210
Ile Leu Glu Lys	Met Asp Ile Phe Leu	Leu Pro Val Ala Asn	Pro
	215	220	225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln	Asn Arg Leu Trp Arg	Lys
	230	235	240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser	Cys Ile Gly Ala Asp	Pro
	245	250	255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala	Gly Lys Gly Ala Ser	Asp
	260	265	270
Asn Pro Cys Ser	Glu Val Tyr His Gly	Pro His Ala Asn Ser	Glu
	275	280	285
Val Glu Val Lys	Ser Val Val Asp Phe	Ile Gln Lys His Gly	Asn
	290	295	300
Phe Lys Gly Phe	Ile Asp Leu His Ser	Tyr Ser Gln Leu Leu	Met
	305	310	315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys	Ala Pro Asp Ala Glu	Glu
	320	325	330
Leu Asp Lys Val	Ala Arg Leu Ala Ala	Lys Ala Leu Ala Ser	Val
	335	340	345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro	Thr Cys Thr Thr Val	Tyr
	350	355	360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp	Ala Tyr Asp Asn Gly	Ile
	365	370	375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg	Asp Thr Gly Thr Tyr	Gly
	380	385	390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile	Pro Thr Ala Glu Glu	Thr
	395	400	405
Trp Leu Gly Leu	Lys Thr Ile Met Glu	His Val Arg Asp Asn	Leu
	410	415	420

Tyr

<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50

tggtccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100



ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150  
cccgcccttc ctccacaaag agcacccttg cctcacaggt gtattccctc 200  
aacaccgact ttgccttccg cctataccgc aggttggttt tggagacccc 250  
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300  
tgctctccct tggggccac tcagtcacca agaccagat tctccagggc 350  
ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400  
ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgaccttga 450  
agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaaat 500  
ttcttgggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550  
tttctccaac ccctccattg cccaggcgag gatcaacagc catgtgaaaa 600  
agaagacca aggaagggtt gtagacataa tccaaggcct tgaccttctg 650  
acggccatgg ttctgggtgaa tcacattttc tttaaagcca agtgggagaa 700  
gccctttcac cttgaatata caagaaagaa cttcccattc ctggtgggcg 750  
agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800  
tttggggtgg atacagagct gaactgcttt gtgctgcaga tggattacaa 850  
gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900  
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ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000  
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cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcacg 1550  
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 aaatacgcca acccaggtta ggcacctcta ttgcagaatt acaataacac 1650  
 attcaataaaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
1				5					10					15

Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
				20					25					30

Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
				35					40					45

Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
				50					55					60

Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
				65					70					75

Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
				80					85					90

Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
				95					100					105

Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
				110					115					120

Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
				125					130					135

Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
				140					145					150

Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
				155					160					165

Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
				170					175					180

Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
				185					190					195

Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala
				200					205					210

Lys Trp Glu Lys	Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctggt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100

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ctttctcaag aatcctctgt tctttgccct cttaaagtctt ggtacatcta 200

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

aaaggaaatg ttctccttat gtttggtcta ctattgcatt tagaagctgc 300  
aacaaattcc aatgagacta gcacctctgc caaacttgga tccagtgtga 350  
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400  
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 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243  
 <211> 596  
 <212> PRT  
 <213> Homo sapiens

<400> 243  
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 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser  
 20 25 30  
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala  
 35 40 45  
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala  
 50 55 60  
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val  
 65 70 75  
 Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala  
 80 85 90  
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala  
 95 100 105

Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	110	115	120
Thr Asn Ser Glu	Ser Ser Thr Pro Ser	Ser Gly Ala Ser Thr	Val
	125	130	135
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ser Gly Ala Ser Thr	Ala
	140	145	150
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Arg Ala Ser Thr	Ala
	155	160	165
Thr Asn Ser Glu	Ser Ser Thr Leu Ser	Ser Gly Ala Ser Thr	Ala
	170	175	180
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	185	190	195
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	200	205	210
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Arg Ala Ser Thr	Ala
	215	220	225
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	230	235	240
Thr Asn Ser Glu	Ser Arg Thr Thr Ser	Asn Gly Ala Gly Thr	Ala
	245	250	255
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	260	265	270
Thr Asn Ser Asp	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala
	275	280	285
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	290	295	300
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	305	310	315
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Gly Ala Gly Thr	Ala
	320	325	330
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val
	335	340	345
Thr Asn Ser Glu	Ser Ser Thr Pro Ser	Ser Gly Ala Asn Thr	Ala
	350	355	360
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala
	365	370	375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala
	380	385	390

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala  
395 400 405

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
410 415 420

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala  
425 430 435

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val  
440 445 450

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala  
455 460 465

Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala  
470 475 480

Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala  
485 490 495

Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile  
500 505 510

Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe  
515 520 525

Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn  
530 535 540

Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly  
545 550 555

Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro  
560 565 570

Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile  
575 580 585

Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro  
590 595

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tggggtaaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgcc accatgctgc 600

tggccaggcc ggggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650

ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700

tccagccatc aaggaggggc cacaaccaag ccgttagcct ctggggcctc 750

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<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

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Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	
Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser	185	190	195	
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser	200	205	210	
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly				

215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg		
230	235	240

Ser Val Ala Asn Ile Met Pro  
245

<210> 249  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 249  
caatatgcat cttgcacgtc tgg 23

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
aagcttctct gcttcctttc ctgc 24

<210> 251  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
tgacccatt gagaaggatc ttgaaggat caaccgagg ctg 43

<210> 252  
<211> 3781  
<212> DNA  
<213> Homo sapiens

<400> 252  
ctccgggtcc ccaggggctg cgcggggccg gcctggcaag ggggacgagt 50  
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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser Phe Lys Gly	Lys Asp Pro Gln Arg	Asp Cys Gln Asn Tyr	Ile
125		130	135
Lys Ile Leu Leu	Pro Leu Ser Gly Ser	His Leu Phe Thr Cys	Gly
140		145	150
Thr Ala Ala Phe	Ser Pro Met Cys Thr	Tyr Ile Asn Met Glu	Asn
155		160	165
Phe Thr Leu Ala	Arg Asp Glu Lys Gly	Asn Val Leu Leu Glu	Asp
170		175	180
Gly Lys Gly Arg	Cys Pro Phe Asp Pro	Asn Phe Lys Ser Thr	Ala
185		190	195
Leu Val Val Asp	Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser	Phe
200		205	210
Gln Gly Asn Asp	Pro Ala Ile Ser Arg	Ser Gln Ser Leu Arg	Pro
215		220	225
Thr Lys Thr Glu	Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala	Phe
230		235	240
Val Ala Ser Ala	Tyr Ile Pro Glu Ser	Leu Gly Ser Leu Gln	Gly
245		250	255
Asp Asp Asp Lys	Ile Tyr Phe Phe Phe	Ser Glu Thr Gly Gln	Glu
260		265	270
Phe Glu Phe Phe	Glu Asn Thr Ile Val	Ser Arg Ile Ala Arg	Ile
275		280	285
Cys Lys Gly Asp	Glu Gly Gly Glu Arg	Val Leu Gln Gln Arg	Trp
290		295	300
Thr Ser Phe Leu	Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp	Asp
305		310	315
Gly Phe Pro Phe	Asn Val Leu Gln Asp	Val Phe Thr Leu Ser	Pro
320		325	330
Ser Pro Gln Asp	Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe	Thr
335		340	345
Ser Gln Trp His	Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys	Val
350		355	360
Phe Thr Met Lys	Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr	Lys
365		370	375
Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His	Pro
380		385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala	Arg
395		400	405

Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
	440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val
	665	670	675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro
	680	685	690



Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys
				695					700					705
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
				710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe
				725					730					735
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln
				740					745					750
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu
				755					760					765
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr
				770					775					780
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro
				785					790					795
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile
				800					805					810
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg
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Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val			
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 254  
 agcccggtgca gaatctgctc ctgg 24

<210> 255  
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 tgaagccagg gcagcgtcct ctgg 24

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<400> 256  
gtacaggctg cagttggc 18

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<212> DNA  
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agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258  
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gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259  
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<213> Homo sapiens

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<221> unsure  
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<223> unknown base

<400> 259  
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agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150  
tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200  
cgcccagagcc gccgctagcg cgcgccgggc atggtccctt cttaaaggcg 250  
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gcggcgctgc ccgggccggg cctcgcggcg ctagggcggg ctggcctccg 400  
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg
				20					25					30
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro
				35					40					45
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
				50					55					60
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
				65					70					75
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
				80					85					90
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
				95					100					105
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
				110					115					120
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
				125					130					135
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
				140					145					150
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
				155					160					165
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
				170					175					180
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
				185					190					195
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
				200					205					210
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
				215					220					225
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
				230					235					240
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val
				245					250					255
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser
				260					265					270
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys

275					280					285				
Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala
				290					295					300
Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu
				305					310					315
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg
				320					325					330
Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser
				335					340					345
Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro
				350					355					360
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu
				365					370					375
Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly
				380					385					390
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu
				395					400					405
Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala
				410					415					420
Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly
				425					430					435
Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp
				440					445					450
Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val
				455					460					465
Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile
				470					475					480
Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys
				485					490					495
Arg	Ile	Asn	Gln	Glu	Ser	Gly	Ser	Leu	Ser	Phe	Leu	Ser	Asn	Ser
				500					505					510
Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu
				515					520					525
His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu
				530					535					540
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu
				545					550					555
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu

560					565					570				
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu
				575					580					585
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln
				590					595					600
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu
				605					610					615
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys
				620					625					630
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg
				635					640					645
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe
				650					655					660
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser
				665					670					675
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn
				680					685					690
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg
				695					700					705
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp
				710					715					720
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe
				725					730					735
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe
				740					745					750
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly
				755					760					765
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met
				770					775					780
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn
				785					790					795
Asn	Gly	Ser	Val	Arg	Thr	Ala								
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<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



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<210> 262  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 262  
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<210> 263  
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<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 263  
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
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gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200  
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60

Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75

Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90

Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335	340	345
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<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20				25					30	

Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu

35					40					45				
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe
				50					55					60
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser
				65					70					75
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr
				95					100					105
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile
				110					115					120
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly
				125					130					135
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile
				140					145					150
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg
				170					175					180
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile
				185					190					195
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu
				200					205					210
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu
				215					220					225
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu
				230					235					240
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile
				245					250					255
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val

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Val Ala Ser Gln Gly Phe Gln Ala Gly	Arg His Tyr Trp Glu Val	
335	340	345
Asp Val Gly Gln Asn Val Gly Trp Tyr	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Gly Lys Asn Asn Val	Thr Leu Ser Pro Asn Asn	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Thr Thr	Glu His Leu Tyr Phe Thr	
380	385	390
Phe Asn Pro His Phe Ile Ser Leu Pro	Pro Ser Thr Pro Pro Thr	
395	400	405
Arg Val Gly Val Phe Leu Asp Tyr Glu	Gly Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Thr Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Leu Thr Cys	
425	430	435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr	Ile Gln His Ala Met Tyr	
440	445	450
Asp Glu Glu Lys Gly Thr Pro Ile Phe	Ile Cys Pro Val Ser Trp	
455	460	465

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 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
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 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
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cca 2103

<210> 269  
<211> 423  
<212> PRT  
<213> Homo sapiens

<400> 269  
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35 40 45  
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
50 55 60  
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
65 70 75  
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
80 85 90  
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
95 100 105  
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
110 115 120  
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
125 130 135  
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
140 145 150  
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
155 160 165  
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
170 175 180  
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
185 190 195  
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
200 205 210

Trp Asp Gly Ser	His Arg Cys Gly Ala	Thr Leu Ile Asn Ala Thr
215		220 225
Trp Leu Val Ser	Ala Ala His Cys Phe	Thr Thr Tyr Lys Asn Pro
230		235 240
Ala Arg Trp Thr	Ala Ser Phe Gly Val	Thr Ile Lys Pro Ser Lys
245		250 255
Met Lys Arg Gly	Leu Arg Arg Ile Ile	Val His Glu Lys Tyr Lys
260		265 270
His Pro Ser His	Asp Tyr Asp Ile Ser	Leu Ala Glu Leu Ser Ser
275		280 285
Pro Val Pro Tyr	Thr Asn Ala Val His	Arg Val Cys Leu Pro Asp
290		295 300
Ala Ser Tyr Glu	Phe Gln Pro Gly Asp	Val Met Phe Val Thr Gly
305		310 315
Phe Gly Ala Leu	Lys Asn Asp Gly Tyr	Ser Gln Asn His Leu Arg
320		325 330
Gln Ala Gln Val	Thr Leu Ile Asp Ala	Thr Thr Cys Asn Glu Pro
335		340 345
Gln Ala Tyr Asn	Asp Ala Ile Thr Pro	Arg Met Leu Cys Ala Gly
350		355 360
Ser Leu Glu Gly	Lys Thr Asp Ala Cys	Gln Gly Asp Ser Gly Gly
365		370 375
Pro Leu Val Ser	Ser Asp Ala Arg Asp	Ile Trp Tyr Leu Ala Gly
380		385 390
Ile Val Ser Trp	Gly Asp Glu Cys Ala	Lys Pro Asn Lys Pro Gly
395		400 405
Val Tyr Thr Arg	Val Thr Ala Leu Arg	Asp Trp Ile Thr Ser Lys
410		415 420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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			20					25						30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40						45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	
				50					55					60	
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	
				65					70					75	
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
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<210> 272  
 <211> 2397  
 <212> DNA  
 <213> Homo sapiens

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atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550  
acttttatta ctacgcgac tattcttctg atgctaaata aattatatat 1600  
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 cttagttagt tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050  
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
			20						25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
			35						40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
			50						55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
			65						70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
			80						85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
			95						100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
			110						115					120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	
				125						130				135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	
				140					145					150	
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	
				155					160					165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	
				170					175					180	
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	
				185					190					195	
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	
				200					205					210	
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	
				215					220					225	
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	
				230					235					240	
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	
				245					250					255	
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	
				260					265					270	
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	
				275					280					285	
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	
				290					295					300	
Glu	Met	Glu	Glu	Leu											
				305											

<210> 274  
 <211> 2063  
 <212> DNA  
 <213> Homo sapiens

<400> 274  
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 cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200  
 agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250  
 cgatgtcaaa cccctgcgca aaccccgatat ccccatggag accttcagaa 300

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attgtggttg tccatcatca ggtgattctg gataaatact acttcctctg 400  
cgggcagcct ctccacttca tcccaggaa gcagctgtgt gacggagagc 450  
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gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550  
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aaacagccag gagcttcgca tgcggaactc aagtggggcc tgtctctcag 750  
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 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850  
 tcaactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900  
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 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000  
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<210> 275  
 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 275  
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 Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg  
 20 25 30  
 Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser  
 35 40 45  
 Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr  
 50 55 60  
 Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln  
 65 70 75  
 Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu  
 80 85 90  
 His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg  
 95 100 105  
 Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr  
 110 115 120  
 Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu  
 125 130 135  
 Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu  
 140 145 150  
 Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn  
 155 160 165  
 Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser  
 170 175 180

Gly Ser Leu Val	Ser Leu His Cys Leu	Ala Cys Gly Lys Ser	Leu
185		190	195
Lys Thr Pro Arg	Val Val Gly Gly Glu	Glu Ala Ser Val Asp	Ser
200		205	210
Trp Pro Trp Gln	Val Ser Ile Gln Tyr	Asp Lys Gln His Val	Cys
215		220	225
Gly Gly Ser Ile	Leu Asp Pro His Trp	Val Leu Thr Ala Ala	His
230		235	240
Cys Phe Arg Lys	His Thr Asp Val Phe	Asn Trp Lys Val Arg	Ala
245		250	255
Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala	Lys
260		265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn	Asp
275		280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly	Thr
290		295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr	Pro
305		310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln	Asn
320		325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln	Val
335		340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly	Glu
350		355	360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly	Val
365		370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln	Ser
380		385	390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly	Cys
395		400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala	Tyr
410		415	420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys	Ala Glu Leu	
425		430	

<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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 caggggtaat ctgagccttc ttcactcctt taccctagct gaccccttca 3050  
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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	

Gly Thr Met Asn	Asn Phe Leu Gly Ser	Glu Pro Ile Leu Met Arg
200		205 210
Thr Leu Gly Ser	Gln Pro Val Leu Lys	Thr Asp Asn Phe Leu Arg
215		220 225
Trp Leu His His	Asp Ala Ser Phe Val	Ala Ala Ile Pro Ser Thr
230		235 240
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe Asp
245		250 255
Phe Phe Glu Arg	Leu His Thr Ser Arg	Val Ala Arg Val Cys Lys
260		265 270
Asn Asp Val Gly	Gly Glu Lys Leu Leu	Gln Lys Lys Trp Thr Thr
275		280 285
Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu Pro
290		295 300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro
305		310 315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val
320		325 330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp
335		340 345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu
350		355 360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg
365		370 375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr
380		385 390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly Thr
395		400 405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val
410		415 420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr
425		430 435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly
440		445 450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp
455		460 465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala
470		475 480

Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg	Ala
485		490	495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg
500		505	510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu
515		520	525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg
530		535	540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser
545		550	555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala
560		565	570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala
575		580	585
Leu Ala Ser Tyr	Tyr Trp Ser His Gly	Pro Ala Ala Val Pro	Glu
590		595	600
Ala Ser Ser Thr	Val Tyr Asn Gly Ser	Leu Leu Leu Ile Val	Gln
605		610	615
Asp Gly Val Gly	Gly Leu Tyr Gln Cys	Trp Ala Thr Glu Asn	Gly
620		625	630
Phe Ser Tyr Pro	Val Ile Ser Tyr Trp	Val Asp Ser Gln Asp	Gln
635		640	645
Thr Leu Ala Leu	Asp Pro Glu Leu Ala	Gly Ile Pro Arg Glu	His
650		655	660
Val Lys Val Pro	Leu Thr Arg Val Ser	Gly Gly Ala Ala Leu	Ala
665		670	675
Ala Gln Gln Ser	Tyr Trp Pro His Phe	Val Thr Val Thr Val	Leu
680		685	690
Phe Ala Leu Val	Leu Ser Gly Ala Leu	Ile Ile Leu Val Ala	Ser
695		700	705
Pro Leu Arg Ala	Leu Arg Ala Arg Gly	Lys Val Gln Gly Cys	Glu
710		715	720
Thr Leu Arg Pro	Gly Glu Lys Ala Pro	Leu Ser Arg Glu Gln	His
725		730	735
Leu Gln Ser Pro	Lys Glu Cys Arg Thr	Ser Ala Ser Asp Val	Asp
740		745	750
Ala Asp Asn Asn	Cys Leu Gly Thr Glu	Val Ala	
755		760	

<210> 278  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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ctgctggtga aatctggcgt ggag 24

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 279  
gtctggtcct ggctgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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catcttgta tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
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cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtgggc 100  
ttccttctcc ctggggtcct gctctcagag gctgccaaaa tcctgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
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<210> 282
<211> 523
<212> PRT
<213> Homo sapiens

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Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
      20             25            30

Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
      35             40            45

Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
      50             55            60

Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
      65             70            75

Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
      80             85            90

Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
      95            100           105

Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
     110            115           120

Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
     125            130           135

Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
     140            145           150

Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile

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155					160					165				
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
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Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly
				260					265					270
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn
				275					280					285
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu
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Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu
				305					310					315
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys
				320					325					330
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn
				335					340					345
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His
				350					355					360
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile
				365					370					375
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu
				380					385					390
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys
				395					400					405
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu
				410					415					420
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser
				425					430					435
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser

440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
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Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
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<210> 283  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 283  
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<210> 284  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 284  
 tcaggctggt ctccaaagag aggg 24

<210> 285  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 286  
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 <212> DNA  
 <213> Homo sapiens

<400> 286  
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cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

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<223> Synthetic oligonucleotide probe

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cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 291  
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<212> DNA  
<213> Homo sapiens

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 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292  
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 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser  
 35 40 45  
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn  
 50 55 60  
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln  
 65 70 75  
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile  
 80 85 90  
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu  
 95 100 105  
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly  
 110 115 120  
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr  
 125 130 135  
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu  
 140 145 150  
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile  
 155 160 165  
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu  
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu	185	190	195
Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser	200	205	210
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu	215	220	225
Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly	230	235	240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr	245	250	255
Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly	260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn	380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

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<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
				20					25					30
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
				35					40					45
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
				50					55					60
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
				65					70					75
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala

80					85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly
				95					100					105
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val
				110					115					120
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr
				125					130					135
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu
				140					145					150
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr
				155					160					165
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe
				170					175					180
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys
				185					190					195
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly
				200					205					210
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val
				215					220					225
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu
				230					235					240
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val
				245					250					255
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala
				260					265					270
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln
				275					280					285
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys
				290					295					300
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala
				305					310					315
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe
				320					325					330
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val
				335					340					345
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu
				350					355					360
Glu Pro Gly Arg Trp Arg Leu Gln														

<210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 298  
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<210> 299  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 299  
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<210> 300  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 300  
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<210> 301  
 <211> 1334  
 <212> DNA  
 <213> Homo sapiens

<400> 301  
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 tgcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100  
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 tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200  
 cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250  
 tagctggggg ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300  
 ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350  
 ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450  
 tgtcgttctt gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500  
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600  
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 ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700  
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 agggcaagg gcattgctgt gcctgccagg tatagtgcct acatgtgggtg 800  
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850  
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 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250  
 gcggagggtg cagtgaagcc agatcaggcc actgtattcc aaccagggtg 1300  
 acagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25						30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40						45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55						60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp



	65		70		75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr					
	80		85		90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln					
	95		100		105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu					
	110		115		120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr					
	125		130		135
Cys Gly Val Leu Leu Ser Phe Leu					
	140				

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
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 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
 tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200  
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
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 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350  
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400  
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 ggcgatggct ccactgccc aggcattcagc cttgctgtag tcaatcactg 550  
 ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600  
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 aattatggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
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Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20					25					30
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro

	65		70		75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala					
	80		85		90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly					
	95		100		105
Arg Arg Arg Asp					

<210> 305  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 305  
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 ccggtctctc gtgcccgcgc cgctggccct gggctcagcc gcaactgggcg 150  
 ccgccttcgc cactggcctc ttctgtggga ggcggtgccc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
 gtatcttctg agccgtcca tgcgggagca cccggcgctg cgaagcctga 300  
 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350  
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 cgctgtcccgc ggacgggcgc gtggtgacct gcgaggtgga cgcgagccc 500  
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 cgacctccgg ctgaagcccg ccttgagagac cctggacgag ctgctggcgg 600  
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 cggcgggacg tcaggggtcta catcagcctc ctgcccctgg gcgatggact 850  
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 gaggggtgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 306

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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu
				65					70					75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln
				80					85					90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys
				95					100					105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu
				110					115					120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val
				125					130					135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala
				140					145					150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu
				155					160					165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp
				170					175					180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr
				185					190					195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val
				200					205					210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly
				215					220					225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg
				230					235					240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly
				245					250					255

Leu Thr Leu Ala Phe Lys Ile  
260

<210> 307  
<211> 2272  
<212> DNA  
<213> Homo sapiens

<400> 307  
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gctaagatga agggctaccc tctctggcct gccaggatcg acgacatcg 150  
ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200  
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250  
aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300  
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cgccagtgag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400  
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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

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Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro	50	55	60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys	65	70	75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala	80	85	90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala	95	100	105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp	110	115	120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala	125	130	135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser	140	145	150
Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser	155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala	170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu	185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala	200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys	215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser	230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser	245	250	255
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val	260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro	275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser	290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu	305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg			

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Glu Lys Glu Glu Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg Gly	
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Glu Ala Glu Arg Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu Arg	
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Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser	
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg	
425	430	435
Pro Glu Glu Lys Gln Gln Ala Lys Pro	Val Lys Val Glu Arg Thr	
440	445	450
Arg Lys Arg Ser Glu Gly Phe Ser Met	Asp Arg Lys Val Glu Lys	
455	460	465
Lys Lys Glu Pro Ser Val Glu Glu Lys	Leu Gln Lys Leu His Ser	
470	475	480
Glu Ile Lys Phe Ala Leu Lys Val Asp	Ser Pro Asp Val Lys Arg	
485	490	495
Cys Leu Asn Ala Leu Glu Glu Leu Gly	Thr Leu Gln Val Thr Ser	
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Gln Ile Leu Gln Lys Asn Thr Asp Val	Val Ala Thr Leu Lys Lys	
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Ile Arg Arg Tyr Lys Ala Asn Lys Asp	Val Met Glu Lys Ala Ala	
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Glu Val Tyr Thr Arg Leu Lys Ser Arg	Val Leu Gly Pro Lys Ile	
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Glu Ala Val Gln Lys Val Asn Lys Ala	Gly Met Glu Lys Glu Lys	
560	565	570
Ala Glu Glu Lys Leu Ala Gly Glu Glu	Leu Ala Gly Glu Glu Ala	
575	580	585
Pro Gln Glu Lys Ala Glu Asp Lys Pro	Ser Thr Asp Leu Ser Ala	
590	595	600
Pro Val Asn Gly Glu Ala Thr Ser Gln	Lys Gly Glu Ser Ala Glu	



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Asp Lys Glu His	Glu Glu Gly Arg Asp	Ser Glu Glu Gly Pro	Arg		
	620	625	630		
Cys Gly Ser Ser	Glu Asp Leu His Asp	Ser Val Arg Glu Gly Pro			
	635	640	645		
Asp Leu Asp Arg	Pro Gly Ser Asp Arg	Gln Glu Arg Glu Arg	Ala		
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 <212> DNA  
 <213> Homo sapiens

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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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				20					25					30

Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45

Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
				50					55					60

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75

Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile
				80					85					90

Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95					100					105

Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110					115					120

Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135

Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150

Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165

Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
				170					175					180

Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185					190					195

Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210

Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215					220					225

His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly

	230		235		240
Ala Lys Phe Ile Gly Thr Phe Phe Ile Pro Asp Thr Tyr Asn Pro	245		250		255
Asp Asp Asp Lys Ile Tyr Phe Phe Phe Arg Glu Ser Ser Gln Glu	260		265		270
Gly Ser Thr Ser Asp Lys Thr Ile Leu Ser Arg Val Gly Arg Val	275		280		285
Cys Lys Asn Asp Val Gly Gly Gln Arg Ser Leu Ile Asn Lys Trp	290		295		300
Thr Thr Phe Leu Lys Ala Arg Leu Ile Cys Ser Ile Pro Gly Ser	305		310		315
Asp Gly Ala Asp Thr Tyr Phe Asp Glu Leu Gln Asp Ile Tyr Leu	320		325		330
Leu Pro Thr Arg Asp Glu Arg Asn Pro Val Val Tyr Gly Val Phe	335		340		345
Thr Thr Thr Ser Ser Ile Phe Lys Gly Ser Ala Val Cys Val Tyr	350		355		360
Ser Met Ala Asp Ile Arg Ala Val Phe Asn Gly Pro Tyr Ala His	365		370		375
Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile	380		385		390
Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro	395		400		405
Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe	410		415		420
Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala	425		430		435
Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr	440		445		450
Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp	455		460		465
Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val	470		475		480
Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu	485		490		495
Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu	500		505		510
Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly					

515					520					525				
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala
				530					535					540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp
				545					550					555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala
				560					565					570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp
				575					580					585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val
				590					595					600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro
				605					610					615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly
				620					625					630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys
				635					640					645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser
				650					655					660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr
				665					670					675
Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu
				680					685					690
Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu
				695					700					705
Leu	Ala	Glu	Ser	Arg	Leu	Arg	Tyr	Lys	Asp	Tyr	Ile	Gln	Ile	Leu
				710					715					720
Ser	Ser	Pro	Asn	Phe	Ser	Leu	Asp	Gln	Tyr	Cys	Glu	Gln	Met	Trp
				725					730					735
His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp
				740					745					750
Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His
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Arg	Asp	Leu	Asp	Glu	Leu	Pro	Arg	Ala	Val	Ala	Thr			
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<212> DNA

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

Met	Gln	Leu	Ala	Lys	Tyr	Gln	Ser	His	Ser	Lys	Ser	Cys	Pro	Thr
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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu
				20					25					30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala
				35					40					45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg
				50					55					60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu
				65					70					75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala
				80					85					90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser
				95					100					105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp
				110					115					120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu
				125					130					135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro
				140					145					150

Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	305	310	315
Pro	Thr	Ser	Val	Leu	Asp	Gly	Pro	Pro	Ala	Pro	Val	Leu	Pro	Gly	320	325	330
Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro	335	340	345
Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala	350	355	360
Pro	Asp	Pro	Gly	His	Pro	Asp	Pro	Leu	Thr						365	370	

<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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				20					25					30	
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
				35					40					45	
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	
				50					55					60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	
				65					70					75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	
				80					85					90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	
				95					100					105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	
				110					115					120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	
				125					130					135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu	
				140					145					150	
Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu	
				155					160					165	
Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile	
				170					175					180	
Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn	
				185					190					195	
Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala	
				200					205					210	
Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val	
				215					220					225	
Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg	
				230					235					240	
Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His	

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Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu Val	
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser Ala	
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu Asn	
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile Leu	
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr Leu	
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser Cys	
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala Ala	
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser Lys	
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His Val	
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp Ser	
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly Tyr	
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu Pro	
425	430	435
Val Thr Phe Pro Gly Lys Asp Tyr Asp	Ala Asp Arg Gln Cys Gln	
440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His	Cys Pro Gln Leu Pro Pro	
455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly	His Leu Asn Gly His Ala	
470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp	Ala Asp Gly Thr Pro Cys	
485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly	Arg Cys Leu His Met Asp	
500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln	Ala Gly Gly Trp Gly Pro	
515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg	Thr Cys Gly Gly Gly Val	



530					535					540				
Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly
				545					550					555
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn
				560					565					570
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu
				575					580					585
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe
				590					595					600
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro
				605					610					615
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr
				620					625					630
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser
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Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala
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Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys
				665					670					675
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly
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Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile
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Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro
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Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser
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Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
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Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
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Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu

815

820

825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys  
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&lt;210&gt; 318

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 318

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&lt;210&gt; 319

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 319

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&lt;210&gt; 320

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 320

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&lt;210&gt; 321

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 321

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<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu
1				5					10					15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

80					85					90				
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe
				95					100					105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys
				110					115					120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro
				125					130					135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe
				140					145					150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn
				155					160					165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn
				170					175					180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu
				185					190					195
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala
				200					205					210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro
				215					220					225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu
				230					235					240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe
				245					250					255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg
				260					265					270
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly
				275					280					285
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys
				290					295					300
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly
				305					310					315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150  
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200  
accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250  
tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300  
tggcgctgcc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350  
tgcctgtctc cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400  
cacgcgtgc gccaaaggga caccgcgcaa gaccaccttt gccatcctcg 450  
gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500  
tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgcccag 550  
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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

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Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

20										25					30				
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser					
				35					40					45					
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly					
				50					55					60					
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln					
				65					70					75					
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu					
				80					85					90					
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr					
				95					100					105					
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu					
				110					115					120					
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala					
				125					130					135					
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro					
				140					145					150					
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr					
				155					160					165					
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu					
				170					175					180					
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln					
				185					190					195					
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala					
				200					205					210					
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val					
				215					220					225					
Thr	Ser	Ala	Thr	His	Ser	Gly	Tyr	Arg	Leu	Asn	Asp	Tyr	Val						
				230					235										

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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aaccccggtca cctccgtggt ccagtagcga gggctctgga ggagctgcgt 250  
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gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350  
gtcctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400  
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ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500  
gtgtttgcca acatgctggg gactaacttc tggatgtcca cagctaacat 550  
gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600  
ttgggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650  
gggggtgtga tgatgtgcat cgcctgccgg ggctggcac cagaagaaac 700  
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800  
aagaagatat acgatggagg tgcccgacac gaggacgagg tacaatctta 850  
tccttccaag cagactatg tgtaatgtc taagacctct cagcacgggc 900  
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950  
atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000  
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050  
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100  
attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150  
gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200  
ccccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250  
tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300  
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cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
cccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa 1450  
agtcattttc agtttgaggc aaccaaact ttctactgct gttgacatct 1500  
tcttattaca gcaacaccat tctaggagt ttctgagctc tccactggag 1550  
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atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650  
 taaaatgata cactatctct gtgaaatagc ctcaccccta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
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 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggctgagg tgggaggatc acttgagccc agggagggtt gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30

Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45

Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60

Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75

Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90

Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105

Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120

Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135

Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150



Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
				155					160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170					175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185					190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200					205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215					220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230					235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
				245					250					255
Ser	Lys	His	Asp	Tyr	Val									
				260										

<210> 327  
 <211> 2010  
 <212> DNA  
 <213> Homo sapiens

<400> 327  
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150  
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200  
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250  
 tgaattgcgt gaggcaggct aacatcagga tgcagtcaa aatctatgat 300  
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350  
 tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttggca 400  
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 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tggtgctcat 500  
 cctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550  
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 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650

tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700  
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 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850  
 caaagaaact ttgattttact gttctttaact gcctaattctt aattacagga 900  
 actgtgcatac agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000  
 taagggtggtt caagcatcta ctctttttat cattttacttc aaaatgacat 1050  
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgtg acattttatat ctccacataga gacatgctta 1150  
 tatggttttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
 actcaactat tgcttttcag ggaaatcatg gatagggttg aagaaggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300  
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400  
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 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500  
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600  
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtat 1650  
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700  
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750  
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800  
 atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850  
 ttttactaaa atctgtaaat actgtat 1900  
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 aatgaatgtg ttctat 2000  
 ttttctaatt 2010

<211> 225  
<212> PRT  
<213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly
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Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp
				20					25					30
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn
				35					40					45
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile
				50					55					60
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met
				80					85					90
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr
				95					100					105
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu
				110					115					120
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile
				125					130					135
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn
				140					145					150
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu
				155					160					165
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala
				170					175					180
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr
				185					190					195
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His
				200					205					210
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329  
<211> 1315  
<212> DNA  
<213> Homo sapiens

<400> 329

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 gaccgctttc atcggaaca gcatcgtgtt ggcccagggt gtgtgggagg 150  
 gcctgtggat gtccctgcgtg gtgcagagca ccggccagat gcagtgaag 200  
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300  
 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350  
 cgctgtgtgc tcacctctgg gattgtcttt gtcatctcag gggctctgac 400  
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 accccttgtt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500  
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 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200  
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250  
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<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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 gttccttggc atgggtgggga ctcttgccac aacccttctg cctcagtggg 200  
 ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250  
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 gcaagttcta tagctccttg ttggctctcc cgctggccct ggaaacagcc 350  
 cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400  
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 ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500  
 atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550  
 tttctacaac ccagccatcc acatagggtca gaaacgagag ctgggagcag 600  
 cacttttcct tggctgggca agcgtctgtg tcctcttcat tggagggggg 650  
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 cgctgctcca attttcatat tctaaattca agtatacca taatcattag 1050  
 caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100  
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 acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
1				5					10					15

Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala	Leu	Met	Cys	Val	Ala	Val	Ala	Leu	Ser	Leu	Ile	Ala	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150

agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200

tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250

gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300

aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350

tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400

ggtagggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

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<210> 334  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 334  
 Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr  
     1                    5                    10                    15  
 Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
                     20                    25                    30  
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
                     35                    40                    45  
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
                     50                    55                    60  
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
                     65                    70                    75  
 Arg Val Gln Phe Leu His Asp Gly Ser Cys  
                     80                    85

<210> 335  
 <211> 742  
 <212> DNA  
 <213> Homo sapiens

<400> 335  
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 ctgctcgcgc cccgccgccg tggtgcctc cccgcgcggg cctgctgtcc 100  
 tggccctgac cgggctggcg ctgctcctgc tctgtgctg gggcccaggt 150  
 ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200  
 tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250  
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 cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350  
 agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400  
 gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450  
 gcaattgggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500  
 ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaatt 550  
 agcgattctc ttcattgtat tcctaattgcc ttacactact tggtttctga 600  
 tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
 gaagagttaa aacaacacat gttaaagcct tttgatattt catgggaatg 700



cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly
1				5					10					15

Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser
			20						25					30

Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val
			35						40					45

Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu
			50						55					60

Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg
			65						70					75

Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met
			80						85					90

Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu
			95						100					105

Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln
			110						115					120

Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr
			125						130					135

Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr
			140						145			

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150

ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200

gacccactgc ccagccgctc agggacccca acgccatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

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ccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacaccca 550
gacctggggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
tgtccacgag agtcgggtccc ccaaataccc cctgcccgcc ggggtccgag 650
cccgccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
ttccccfgac cgccactctg ggcttgccg gcttcaccct gtcctcagt 800
ctcctggcct ttgccatgta ccgcccgtag tgctccgcg ggcgcttggc 850
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ctgcctgccc agggccgcct ctccggcctg cctcttcccg ctgccctgga 950
gccagccct gcgcgcgaga ggactcccgg gactggcgga gggcccgccc 1000
tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
cgcaactggga gtgggtcct cggggtcggg catctgctgt cgctgcctcg 1100
gccccgggca gagccggggc gccccggggg ccgctcttag tgttctgccg 1150
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acgccaggtc ggtgggaggc tggatgaagg gagcggggag gggcagagga 1250
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<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

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Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
  1               5               10               15
Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
                20                25                30
Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
                35                40                45

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Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300  
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
 tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400  
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500  
 gtccggagca cgggggatga acaactgggt agaatggagg ttgcaactgtt 550  
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 aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
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 ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750  
 tcttggttc ctccttactc ccatctggac ccagtcacct ggttcctgtc 800  
 tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala	1	5	10	15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val	20	25	30	
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser	35	40	45	
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser	50	55	60	
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe	65	70	75	
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser	80	85	90	
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn	95	100	105	
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala	110	115	120	
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly	125	130	135	

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg  
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

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<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

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<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

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<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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actgagaacc caccagctca tccagacac ctcatagcaa cctatttata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccggggtaaa gggagggag caattcaatt tgaagtcct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300  
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gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500  
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 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900  
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 gctgtcaggc aggagcagg tattcttcag aactgcacgg aggaaggcct 2200  
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 atatatttca tgaagctgat ctttttgtgt gtgtgtcct tgtgttagga 2500  
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly
				260					265					270



Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala	His
	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg	Ile
	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val	Ile
	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln	Arg
	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu	Pro
	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile	Arg
	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His	Tyr
	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg	Gly
	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly	Gly
	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr	Gln
	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu	Arg
	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys	Glu
	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys	Ala
	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg	Leu
	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro	Glu
	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu	His
	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly	Asp
	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser	Arg
	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His	Phe
	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val
				560					565					570
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln
				575					580					585
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser
				590					595					600
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu
				605					610					615
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe
				620					625					630
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg						
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<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 348  
 ggagaggtgg tggccatgga cag 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 349  
 ctgtcactgc aaggagccaa cacc 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 350  
 tatgtcgctg cgaggtggtg aaaacctga actgtctttc aaggc 45

<210> 351  
 <211> 2524  
 <212> DNA  
 <213> Homo sapiens

<400> 351

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tcctctcttg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgctc 200  
caggggaggg ccctcggccc caggtcatgt gtgcgtgtgg gagcgagcac 250  
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cctggcactg cccccccagc ccccccatca ggctttgagg agggggccgcc 350  
ctcatcccaa taccctggg ctatcgtgtg gggteccacc gtgtctcgag 400  
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tttgagccc ctcatgggct cgcaaccca caccacaact cagactccat 500  
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cacaccaccc ggaacactcc ccagccccac gggcaatcct atctgctcgc 1450  
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tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1.				5				10						15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20				25						30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggtcgc tggggcccg cgctatcgcg gccatcgtga 350  
 tcgccgcct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser  
 1 5 10 15  
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu  
 20 25 30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
 35 40 45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
 50 55 60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
 65 70 75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
 80 85 90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
 95 100 105  
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
 110 115 120  
 Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
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 gttggccggc ggcggggccg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150  
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200  
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300  
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400  
catcttcggg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500  
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550  
agtagccccc agaggcgctg ggagtgttgc caccgcctc ccctgaagtt 600  
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650  
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700  
tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750  
acgtcgctg ctttggctat aactgcgagt agggctcagg catcacaccc 800  
accctgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850  
gggtccccc ccttcacct ggctgtcacc gggtagggcg gggcctggg 900  
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tggaagtcag ctgtccagg cctcctgaac tacataaata actggcacia 1000  
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
cgtgggtgag tatgtgtgg gcacaggctg gctccctcag ctcccacgtc 1100  
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gcggctgcag tccttttctc cctcaaaggc ctccgacct cagctggagg 1200  
cgggcatctt tcctaaagg tcccatagg gtctggttcc acccatccc 1250  
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ccatggaggg gctgactgcc ccacattgcc ttccagacag gacacgagca 1350  
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acccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550  
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 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650  
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 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000  
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050  
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100  
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
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His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
				20					25					30
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
				35					40					45
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
				50					55					60
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
				65					70					75
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
				80					85					90
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
				95					100					105
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
				110					115					120
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln



	125		130		135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro					
	140		145		150
Ser Pro Arg Gly Asp Leu Pro					
	155				

<210> 357  
 <211> 1536  
 <212> DNA  
 <213> Homo sapiens

<400> 357  
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 ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cacgtggctc 150  
 acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200  
 cataggett cttcaggatt tagaaatacc agcagtgcc atactccata 250  
 gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300  
 gaggtttctga cacactacaa catcactggg aacaccatct gcctctttcg 350  
 cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400  
 ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450  
 gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500  
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 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600  
 ctctttattc tgggtggacag tggatatgaaa gaaaatggga aggtgatatc 650  
 atttttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700  
 ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750  
 catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800  
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850  
 ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900  
 aactcaaate tcagagacac taaacaacag gatcactagg cctgcccaacc 950  
 acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000  
 gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050  
 tctcttcttc cttcttttaa atttcatatc ctcactccct atccaatttc 1100

ctcttattcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150  
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 ctagagaaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
 cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300  
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
 tcaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400  
 cagaagttaa aggtgtctc caagtcctc aactcagcag aaatagacca 1450  
 tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500  
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
			20					25						30

Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
			35					40						45

Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
			50					55						60

Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
			65					70						75

His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
			80					85						90

Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
			95					100						105

Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
			110					115						120

Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
			125					130						135

Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
			140					145						150

Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
			155					160						165

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 359  
 ccagcagtgc ccatactcca tagc 24

<210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 360  
 tgacgagtgg gatacactgc 20

<210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 361  
 gctctacgga aacttctgct gtgg 24

<210> 362  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50  
ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagcaa 100  
cctcagcggg gaccgggct cagggacgcg gggcgggcgg cggcgactgc 150  
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200  
cccagacagc cggcgctggc tgtggtcggg gctggcggcg gcgcttgggc 250  
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300  
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcgggttga cctcagtcct ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550  
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600  
cctggacaca ttaggctcta tgcgtagaa aaagagaatt tgcctgtgtt 650  
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggctctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800  
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
tgcttcttgg atctcaccag ggcccagtcata tatatgcaca gttagaccac 900  
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
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 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
 cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200  
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350  
 ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400  
 tggaggatgg agatgctatg atggaagcat acccaggggt gccttttagca 1450  
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccattggg 1500  
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550  
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700  
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
 cgtggagagt aaaaagtatc gggtttta 1777

<210> 364  
 <211> 269  
 <212> PRT  
 <213> Homo sapiens

<400> 364  
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp  
 1 5 10 15  
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu  
 20 25 30  
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu  
 35 40 45  
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe  
 50 55 60  
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
 65 70 75  
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
 80 85 90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp
				95					100					105
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
				110					115					120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
				125					130					135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
				140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val
				155					160					165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr
				170					175					180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn
				185					190					195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser
				200					205					210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly
				215					220					225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile
				230					235					240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile
				245					250					255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn	
				260					265					

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

gccggctgtg cagagacgcc atgtaccggc tctgtgcagc agtgactgcc 50

cgggctgccg cccccggggg cttggcctca agctgcgga cgcgcgggt 100

ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcgggggcc 150

tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200

aggggcgcgg ccccggcgca gtccccgcg gccccgacc ctgaggcgtc 250

gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctcgc 300

agaccccgcc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350

agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400

agtgggttga gtttctgtag atggaaaaga agtctgggtca gaaggttttag 450  
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500  
 cgaattgcta gcatcagcaa aagtctcacc atgggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
 agattactga tttccatttt aagtgggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaacctt ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000  
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaataatt 1050  
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
 caggaagaaa acgagccagt gatttacaat agagcaagggt aaatgaatac 1150  
 cttctgctgt gtctagctat atcgcatott aacactattt tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5				10					15	

Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20				25					30	

Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35				40					45	

Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50				55					60	

Arg Gly Ala Ala	Pro Ala Gln Ser Pro	Ala Ala Pro Asp Pro	Glu
65	70		75
Ala Ser Pro Leu	Ala Glu Pro Pro Gln	Glu Gln Ser Leu Ala	Pro
80	85		90
Trp Ser Pro Gln	Thr Pro Ala Pro Pro	Cys Ser Arg Cys Phe	Ala
95	100		105
Arg Ala Ile Glu	Ser Ser Arg Asp Leu	Leu His Arg Ile Lys	Asp
110	115		120
Glu Val Gly Ala	Pro Gly Ile Val Val	Gly Val Ser Val Asp	Gly
125	130		135
Lys Glu Val Trp	Ser Glu Gly Leu Gly	Tyr Ala Asp Val Glu	Asn
140	145		150
Arg Val Pro Cys	Lys Pro Glu Thr Val	Met Arg Ile Ala Ser	Ile
155	160		165
Ser Lys Ser Leu	Thr Met Val Ala Leu	Ala Lys Leu Trp Glu	Ala
170	175		180
Gly Lys Leu Asp	Leu Asp Ile Pro Val	Gln His Tyr Val Pro	Glu
185	190		195
Phe Pro Glu Lys	Glu Tyr Glu Gly Glu	Lys Val Ser Val Thr	Thr
200	205		210
Arg Leu Leu Ile	Ser His Leu Ser Gly	Ile Arg His Tyr Glu	Lys
215	220		225
Asp Ile Lys Lys	Val Lys Glu Glu Lys	Ala Tyr Lys Ala Leu	Lys
230	235		240
Met Met Lys Glu	Asn Val Ala Phe Glu	Gln Glu Lys Glu Gly	Lys
245	250		255
Ser Asn Glu Lys	Asn Asp Phe Thr Lys	Phe Lys Thr Glu Gln	Glu
260	265		270
Asn Glu Ala Lys	Cys Arg Asn Ser Lys	Pro Gly Lys Lys Lys	Asn
275	280		285
Asp Phe Glu Gln	Gly Glu Leu Tyr Leu	Arg Glu Lys Phe Glu	Asn
290	295		300
Ser Ile Glu Ser	Leu Arg Leu Phe Lys	Asn Asp Pro Leu Phe	Phe
305	310		315
Lys Pro Gly Ser	Gln Phe Leu Tyr Ser	Thr Phe Gly Tyr Thr	Leu
320	325		330
Leu Ala Ala Ile	Val Glu Arg Ala Ser	Gly Cys Lys Tyr Leu	Asp
335	340		345



Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val  
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg  
365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

tggaagaa gtctggcag aaggttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttgctt cattctcctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgcacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
 ctggggcaac ccggtgctc ctgctcttgc tgatggcggt agcagcgccc 150  
 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
 tggggcggaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
 tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300  
 tcaactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350  
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
 gaagctggtg gctatgtctc ctcttttgc cctgcgtgct ccctggtgga 500  
 gtgcacactg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
 tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600  
 gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650  
 gcccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgctgg 700  
 agatggaaca ggcccagaag gccagaacc cccaggagca gaagtccttc 750  
 ttgcgcaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800  
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850  
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900  
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
 agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000  
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5				10					15	

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20					25					30	

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	35	40	45
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150  
tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200  
ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250  
ctggactttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300  
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggte 350  
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400  
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450  
cctctttctcc ctgacttact cactatgctg cttaaccaa ctctctcaag 500  
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550  
ctgctcttct cagccttcga ggccctggtat atccatgagc acgtggaacg 600  
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650  
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gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750  
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ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
cagcatttgc tctgctgtca tggatggc tctgctggca gtggtgggac 1400  
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
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gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaaggtgc caaaagttcc 1650  
 ctctgtgtta ctccattta gaaaataaac acttttaaata gatcaaaaaa 1700  
 aaaaaa 1706

<210> 374  
 <211> 450  
 <212> PRT  
 <213> Homo sapiens

<400> 374  
 Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser  
 1 5 10 15  
 Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly  
 20 25 30  
 Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe  
 35 40 45  
 Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala  
 50 55 60  
 Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly  
 65 70 75  
 Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu  
 80 85 90  
 Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys  
 95 100 105  
 Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu  
 110 115 120  
 Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala  
 125 130 135  
 Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala  
 140 145 150  
 Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu  
 155 160 165  
 Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val  
 170 175 180  
 Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp  
 185 190 195  
 Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu  
 200 205 210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile
				245					250					255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp
				260					265					270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe
				275					280					285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg
				290					295					300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu
				305					310					315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr
				320					325					330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile
				335					340					345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser
				350					355					360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala
				365					370					375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys
				380					385					390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr
				395					400					405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu
				410					415					420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu
				425					430					435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu
				440					445					450

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

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 gctccccgcg tgcgtcgcgg ccacaggctt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgccaagg actttggtgg tatctttcac acaaggatg agcagattca 250  
 ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300  
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350  
 ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
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 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650  
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgagaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750  
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 gctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccagggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
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 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

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Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25					30	

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40					45	

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr	
				50					55					60	
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly	
				65					70					75	
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val	
				80					85					90	
Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln	
				95					100					105	
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
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 ctgaacaaga tggatcaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gggactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagaccatg actgctgcta tgaccacctg 250  
 aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400



aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
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Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30

Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45

Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60

Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75

Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90

His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105

Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu
			110						115	

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 381  
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<210> 382  
<211> 764  
<212> DNA  
<213> Homo sapiens

<400> 382  
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gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
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gactcctggg acgtgaaact gggagcctta ggtgggaata cccagggaagt 350  
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ggtatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700  
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gcttctgcag aaaa 764

<210> 383  
<211> 178  
<212> PRT  
<213> Homo sapiens

<400> 383  
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1 5 10 15

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Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr	35	40	45
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	50	55	60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	65	70	75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	80	85	90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	95	100	105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	110	115	120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	125	130	135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	140	145	150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	155	160	165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			170	175	

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

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atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatc 150
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
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tgtcagcgag ccctgactca ctacagtgca gctgacaggg gctgtcatgc 450

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<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala
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Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala
				20					25					30

Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val
				35					40					45

Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser
				50					55					60

Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys
				65					70					75

Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu
				80					85					90

Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe
				95					100					105

Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg
				110					115					120

Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu
				125					130					135

Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser
				140					145					150

Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu	200	205	210
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe	215	220	225
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys	230	235	240
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu	245	250	255
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly	260	265	270
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu	275	280	285
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser	290	295	300
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu	305	310	315
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe	320	325	330
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu	335	340	345
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile	350	355	360
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu	365	370	375
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu	380	385	390
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly	395	400	405
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile	410	415	420
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu	425	430	435

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys  
440 445 450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys  
455 460 465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr  
470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu  
485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
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Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gctgagtta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
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aacaccctaa tggctgggtat atctggatcc tcctgctgct ggttttggtg 250  
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<210> 390  
<211> 146  
<212> PRT  
<213> Homo sapiens

<400> 390  
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Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln  
35 40 45  
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Leu Val Leu  
50 55 60  
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys  
65 70 75  
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala  
80 85 90  
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala  
95 100 105  
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro  
110 115 120  
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser  
125 130 135  
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr  
140 145

<210> 391  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 391  
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<210> 392  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

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<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

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accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100  
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250  
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cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350  
ttttcaagtc ttgatttggt gcttacctca agttaccatt tttcagtcaa 400  
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450  
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatattggg 500  
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550  
gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600  
tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650  
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700  
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gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800  
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850  
ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900  
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950

aagctctaca catttttcaag gagtatgctg gattcatgga actctaattc 1000  
tgtacataaa aatttttaaag ttatttgttt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100  
aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150  
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taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900  
attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950  
tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000  
accctaattc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050  
atttcccttg tagcaaattc aattgccaca tgggtgcccta tatttcatag 2100  
tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150  
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200  
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250  
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acctttatgt gaagaaatta attatatgcc attgccaggt 2340

<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 395  
Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser  
1 5 10 15  
Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu  
20 25 30  
His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
35 40 45  
Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
50 55 60  
Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
65 70 75  
Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
80 85 90  
Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
95 100 105  
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
110 115 120  
Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
125 130 135  
Ser Gly Ser Ile Arg  
140

<210> 396  
<211> 2639  
<212> DNA  
<213> Homo sapiens

<400> 396  
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tccagcccc accatgccgt ggcacctgct gctgctgctg gccgtgagtg 100  
gggcccagac aaccgcggca tgcttccccg ggtgccaatg cgaggtggag 150  
accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
tggaacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300  
gggcccgggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
caccagcatc tcaccactg ccttctcccg ccttcgctac ctggagtcgc 400

ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500  
ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550  
acctctccca caacctcatt caccgcctcg tgccccaccc cacgagggcc 600  
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ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700  
atgggaaccc tctagctgtc attggtccgg gtgccttcgc ggggctggga 750  
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gccagtggc ttccgtgagc taccgggcct gcaggctcctg gacctgtcgg 850  
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ggcgctgctc ctccacctcc cggcactgca gagcgtcagc gtgggccagg 1000  
atgtgcggtg ccggcgccctg gtgcgggagg gcacctaccc ccggaggcct 1050  
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tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150  
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ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400  
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tgggctgagt gtccccttgg gcccatggcc cagtcaactca ggggcgagtt 1550  
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cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900  
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ccccacaggg cagtgaagtc tgtcttcccc cacctgccta gcccatcatc 2550  
tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln
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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe	Ser
	95	100	105
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly	Leu
	110	115	120
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser	Asp
	125	130	135
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser	Ala
	140	145	150
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu	Ser
	155	160	165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala	Gly
	170	175	180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn	Arg
	185	190	195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr	Leu
	200	205	210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala	Phe
	215	220	225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu	Gln
	230	235	240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro	Gly
	245	250	255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp	Ala
	260	265	270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu	Asp
	275	280	285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu	Leu
	290	295	300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val	Arg
	305	310	315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro	Gly
	320	325	330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu	Ser
	335	340	345
Ala Ala Arg Gly	Pro Thr Ile Leu		
	350		

<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagctt acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

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ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550



gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600  
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 aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700  
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 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850  
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 gatgctctgt gagatatattg aaattgaacc aatgactact taggatgggt 1400  
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
 ccattcccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
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 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20					25					30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35					40					45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	50	55	60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	65	70	75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	80	85	90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50  
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgcgcac ttacagacac gtagtgtatt ctggaggctc aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aatcagtc tttggaggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
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gctgggtacc caatatacaa agagcagcac tgggtaatat gggagattta 650  
accacttatg atacagtga aactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aagggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtc agaatgaccc cttggtcaat ggtgttctgg 950  
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<210> 406  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln	1	5	10	15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	20	25	30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	35	40	45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	50	55	60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	65	70	75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	80	85	90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	95	100	105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	110	115	120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	125	130	135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	140	145	150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	155	160	165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	170	175	180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	185	190	195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	200	205	210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	215	220	225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	230	235	240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	245	250	255	

Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	260	265	270
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	275	280	285
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	290	295	300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	305	310	315
Glu	Met	Ser	Gly	Val	Ser	Pro	Phe								320		

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

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<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

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tagataattt tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200

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accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcattg 350

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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
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Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
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Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
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<210> 412  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 412  
 ccaaactcga gcacctgttc 20

<210> 413  
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<220>  
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<210> 414  
<211> 1337  
<212> DNA  
<213> Homo sapiens

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<210> 415

<211> 224

<212> PRT

<213> Homo sapiens

<400> 415

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				20					25					30

Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr
				35					40					45

Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro
				50					55					60

Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala
				65					70					75

Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met
				80					85					90

Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu
				95					100					105

Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp
				110					115					120

Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu
				125					130					135

Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro
				140					145					150

Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu
				155					160					165

Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val
				170					175					180

Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln
				185					190					195

Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro
				200					205					210

Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	
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<220>  
<223> Synthetic oligonucleotide probe

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<210> 417  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 417  
ggatggccag agctgctg 18

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<400> 418  
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<210> 421

<211> 46  
<212> DNA  
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<220>  
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<400> 421  
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<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
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cacgccagga gctcgctcgc tctctctctc tctctctcac tctcctctcc 200  
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 t 1701

<210> 423  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

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 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
 35 40 45  
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
 50 55 60  
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
 65 70 75  
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu  
 80 85 90

Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala	95	100	105
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly	110	115	120
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His	125	130	135
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala	140	145	150
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu	155	160	165
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His	170	175	180
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro	185	190	195
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe	200	205	210
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val	215	220	225
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln	230	235	240
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro	245	250	255
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn	260	265	270
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr	275	280	285
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly	290	295	300
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile	305	310	315
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser	320	325	330
Ala	Gln	Ala	Thr	Thr	Glu	Ala									335		

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 424  
gtaaagtcgc tggccagc 18

<210> 425  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 425  
cccgatctgc ctgctgta 18

<210> 426  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 426  
ctgcactgta tggccattat tgtg 24

<210> 427  
<211> 45  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 427  
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428  
<211> 1073  
<212> DNA  
<213> Homo sapiens

<400> 428  
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<210> 429  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 429  
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 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn  
 35 40 45  
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu  
 50 55 60  
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met  
 65 70 75  
 Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn  
 80 85 90  
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr

	95	100	105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu	Ser Ser Glu Glu Leu	Pro
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Gln Ile Phe Thr	Ser Leu Ile Ile His	Ser Leu Phe Pro Gly	Gly
	125	130	135
Ile Leu Pro Thr	Ser Gln Ala Gly Ala	Asn Pro Asp Val Gln	Asp
	140	145	150
Gly Ser Leu Pro	Ala Gly Gly Ala Gly	Val Asn Pro Ala Thr	Gln
	155	160	165
Gly Thr Pro Ala	Gly Arg Leu Pro Thr	Pro Ser Gly Thr Asp	Asp
	170	175	180
Asp Phe Ala Val	Thr Thr Pro Ala Gly	Ile Gln Arg Ser Thr	His
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<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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tccaaca 1257

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<400> 431

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Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
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Leu Pro Lys

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cgagtgtgtg cgaaacctaa 20

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aaggccaagg tgagtccat 19

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-230-

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